

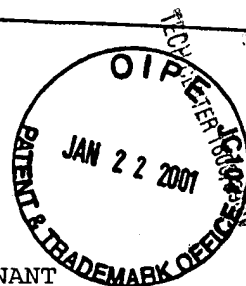
SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: MARIA DIAZ-TORRES ET AL.
- (ii) TITLE OF INVENTION: METHOD FOR THE RECOMBINANT  
PRODUCTION OF 1,3 PROPANEDIOL
- (iii) NUMBER OF SEQUENCES: 68
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Genencor International, Inc.  
(B) STREET: 4 Cambridge Place  
1870 South Winton road  
(C) CITY: Rochester  
(D) STATE: NY  
(E) COUNTRY: U.S.A  
(F) ZIP: 14618
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: Windows  
(D) SOFTWARE: FastSEQ for Windows Version 2.0b
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/969,683  
(B) FILING DATE: 13-NOV-1997  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 60/030,601  
(B) FILING DATE: 13-NOV-1996
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Glaister, Debra  
(B) REGISTRATION NUMBER: 33,888  
(C) REFERENCE/DOCKET NUMBER: GC 369-2
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 650-864-7620  
(B) TELEFAX: 650-845-6504  
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1668 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear



RECEIVED  
JAN 23 1 2001

a!

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: DHAB1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAAAAGAT CAAAACGATT TGCAGTACTG GCCCAGCGCC CCGTCAATCA GGACGGGCTG	60
ATTGGCGAGT GGCCTGAAGA GGGGCTGATC GCCATGGACA GCCCCTTTGA CCCGGTCTCT	120
TCAGTAAAAG TGGACAACGG TCTGATCGTC GAACTGGACG GCAAACGCCG GGACCAGTTT	180
GACATGATCG ACCGATTTAT CGCCGATTAC GCGATCAACG TTGAGCGCAC AGAGCAGGCA	240
ATGCGCCTGG AGGCGGTGGA AATAGCCCGT ATGCTGGTGG ATATTACAGT CAGCCGGGAG	300
GAGATCATTG CCATCACTAC CGCCATCACG CCGGCCAAAG CGGTCGAGGT GATGGCGCAG	360
ATGAACGTGG TGGAGATGAT GATGGCGCTG CAGAAGATGC GTGCCCCCGG GACCCCTCC	420
AACCAGTGCC ACGTCACCAA TCTCAAAGAT AATCCGGTGC AGATTGCCGC TGACGCCGCC	480
GAGGCCGGGA TCCGCGGCTT CTCAGAACAG GAGACCACGG TCGGTATCGC GCGCTACCG	540
CCGTTTAACG CCCTGGCGCT GTTGGTCGGT TCGCAGTGCG GCCGCCCGG CGTGTTGACG	600
CAGTGCTCGG TGGAAGAGGC CACCGAGCTG GAGCTGGGCA TCGTGCGCTT AACCAGCTAC	660
GCCGAGACGG TGTCGGTCTA CGGCACCGAA GCGGTATTTA CCGACGGCGA TGATACGCCG	720
TGGTCAAAGG CGTTCCTCGC CTCGGCCTAC GCCTCCCGCG GGTGAAAAT GCGCTACACC	780
TCCGGCACCG GATCCGAAGC GCTGATGGGC TATTCGGAGA GCAAGTCGAT GCTCTACCTC	840
GAATCGCGCT GCATCTTCAT TACTAAAGGC GCCGGGGTTC AGGGACTGCA AAACGGCGCG	900
GTGAGCTGTA TCGGCATGAC CGGCGCTGTG CCGTCGGGCA TTCGGGCGGT GCTGGCGGAA	960
AACCTGATCG CCTCTATGCT CGACCTCGAA GTGGCGTCCG CCAACGACCA GACTTTCTCC	1020
CACTCGGATA TTCGCCGCAC CGCGCGCACC CTGATGCAGA TGCTGCCGGG CACCGACTTT	1080
ATTTTCTCCG GCTACAGCGC GGTGCCGAAC TACGACAACA TGTTCCGGG CTCGAACTTC	1140
GATGCGGAAG ATTTTGATGA TTACAACATC CTGCAGCGTG ACCTGATGGT TGACGGCGGC	1200
CTGCGTCCGG TGACCGAGGC GGAAACCATT GCCATTCGCC AGAAAGCGGC GCGGGCGATC	1260
CAGGCGGTTT TCCGCGAGCT GGGGCTGCCG CCAATCGCCG ACGAGGAGGT GGAGGCCGCC	1320
ACCTACGCGC ACGGCAGCAA CGAGATGCCG CCGCGTAACG TGGTGGAGGA TCTGAGTGCG	1380

GTGGAAGAGA TGATGAAGCG CAACATCACC GGCCTCGATA TTGTCGGCGC GCTGAGCCGC 1440  
AGCGGCTTTG AGGATATCGC CAGCAATATT CTCAATATGC TGCGCCAGCG GGTCACCGGC 1500  
GATTACCTGC AGACCTCGGC CATTCTCGAT CGGCAGTTCG AGGTGGTGAG TGCGGTCAAC 1560  
GACATCAATG ACTATCAGGG GCCGGGCACC GGCTATCGCA TCTCTGCCGA ACGCTGGGCG 1620  
GAGATCAAAA ATATTCCGGG CGTGGTTCAG CCCGACACCA TTGAATAA 1668

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 585 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: DHAB2

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGCAACAGA CAACCCAAAT TCAGCCCTCT TTTACCTGA AAACCCGCGA GGGCGGGGTA 60  
GCTTCTGCCG ATGAACGCGC CGATGAAGTG GTGATCGGCG TCGGCCCTGC CTTGATAAA 120  
CACCAGCATC ACACTCTGAT CGATATGCCC CATGGCGCGA TCCTCAAAGA GCTGATTGCC 180  
GGGGTGGAAG AAGAGGGGCT TCACGCCCCG GTGGTGCGCA TTCTGCGCAC GTCCGACGTC 240  
TCCTTTATGG CCTGGGATGC GGCCAACCTG AGCGGCTCGG GGATCGGCAT CGGTATCCAG 300  
TCGAAGGGGA CCACGGTCAT CCATCAGCGC GATCTGCTGC CGCTCAGCAA CCTGGAGCTG 360  
TTCTCCCAGG CGCCGCTGCT GACGCTGGAG ACCTACCGGC AGATTGGCAA AAACGCTGCG 420  
CGCTATGCGC GCAAAGAGTC ACCTTCGCCG GTGCCGGTGG TGAACGATCA GATGGTGCGG 480  
CCGAAATTTA TGGCCAAAGC CGCGCTATTT CATATCAAAG AGACCAAACA TGTGGTGCAG 540  
GACGCCGAGC CCGTCACCCT GCACATCGAC TTAGTAAGGG AGTGA 585

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 426 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:

(A) ORGANISM: DHAB3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
ATGAGCGAGA AAACCATGCG CGTGCAGGAT TATCCGTTAG CCACCCGCTG CCCGGAGCAT    60
ATCCTGACGC CTACCGGCAA ACCATTGACC GATATTACCC TCGAGAAGGT GCTCTCTGGC    120
GAGGTGGGCC CGCAGGATGT GCGGATCTCC CGCCAGACCC TTGAGTACCA GGCGCAGATT    180
GCCGAGCAGA TGCAGCGCCA TGCGGTGGCG CGCAATTTCC GCCGCGCGGC GGAGCTTATC    240
GCCATTCTTG ACGAGCGCAT TCTGGCTATC TATAACGCGC TCGCGCCGTT CCGCTCCTCG    300
CAGGCGGAGC TGCTGGCGAT CGCCGACGAG CTGGAGCACA CCTGGCATGC GACAGTGAAT    360
GCCGCCTTTG TCCGGGAGTC GCGGGAAGTG TATCAGCAGC GGCATAAGCT GCGTAAAGGA    420
AGCTAA                                           426
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1164 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: DHAT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
ATGAGCTATC GTATGTTTGA TTATCTGGTG CCAAACGTTA ACTTTTTTTGG CCCCACGCC    60
ATTTCCGTAG TCGGCGAACG CTGCCAGCTG CTGGGGGGGA AAAAAGCCCT GCTGGTCACC    120
GACAAAGGCC TCGGGGCAAT TAAAGATGGC GCGGTGGACA AAACCCTGCA TTATCTGCGG    180
GAGGCCGGGA TCGAGGTGGC GATCTTTGAC GGCGTCGAGC CGAACCCGAA AGACACCAAC    240
GTGCGCGACG GCCTCGCCGT GTTTCGCCGC GAACAGTGCG ACATCATCGT CACCGTGGGC    300
GGCGGCAGCC CGCACGATTG CGGCAAAGGC ATCGGCATCG CCGCCACCCA TGAGGGCGAT    360
CTGTACCAGT ATGCCGGAAT CGAGACCCTG ACCAACCCGC TGCCGCCTAT CGTCGCGGTC    420
AATACCACCG CCGGCACCGC CAGCGAGGTC ACCCGCCACT GCGTCCTGAC CAACACCGAA    480
ACCAAAGTGA AGTTTGTGAT CGTCAGCTGG CGCAAACCTGC CGTCGGTCTC TATCAACGAT    540
CCACTGCTGA TGATCGGTAA ACCGGCCGCC CTGACCGCGG CGACCGGGAT GGATGCCCTG    600
ACCCACGCCG TAGAGGCCTA TATCTCCAAA GACGCTAACC CGGTGACGGA CGCCGCCGCC    660
```

ATGCAGGCGA TCCGCCTCAT CGCCCGCAAC CTGCGCCAGG CCGTGGCCCT CGGCAGCAAT	720
CTGCAGGCGC GGGAAAACAT GGCCTATGCT TCTCTGCTGG CCGGGATGGC TTTCAATAAC	780
GCCAACCTCG GCTACGTGCA CGCCATGGCG CACCAGCTGG GCGGCCTGTA CGACATGCCG	840
CACGGCGTGG CCAACGCTGT CCTGCTGCCG CATGTGGCGC GCTACAACT GATCGCCAAC	900
CCGGAGAAAT TCGCCGATAT CGCTGAACTG ATGGGCGAAA ATATCACCGG ACTGTCCACT	960
CTCGACGCGG CGGAAAAAGC CATCGCCGCT ATCACGCGTC TGTCGATGGA TATCGGTATT	1020
CCGCAGCATC TGCGCGATCT GGGGGTAAAA GAGGCCGACT TCCCCTACAT GGCAGGATG	1080
GCTCTAAAAG ACGGCAATGC GTTCTCGAAC CCGCGTAAAG GCAACGAGCA GGAGATTGCC	1140
GCGATTTTCC GCCAGGCATT CTGA	1164

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1380 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: GPD1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTTTAATTTT CTTTATCTT ACTCTCCTAC ATAAGACATC AAGAAACAAT TGTATATTGT	60
ACACCCCCC CCTCCACAAA CACAAATATT GATAATATAA AGATGTCTGC TGCTGCTGAT	120
AGATTAAACT TAACTTCCGG CCACTTGAAT GCTGGTAGAA AGAGAAGTTC CTCTTCTGTT	180
TCTTTGAAGG CTGCCGAAAA GCCTTTCAAG GTTACTGTGA TTGGATCTGG TAACTGGGGT	240
ACTACTATTG CCAAGGTGGT TGCCGAAAAT TGTAAGGGAT ACCCAGAAGT TTTCGCTCCA	300
ATAGTACAAA TGTGGGTGTT CGAAGAAGAG ATCAATGGTG AAAAATTGAC TGAAATCATA	360
AATACTAGAC ATCAAAACGT GAAATACTTG CCTGGCATCA CTCTACCCGA CAATTTGGTT	420
GCTAATCCAG ACTTGATTGA TTCAGTCAAG GATGTCGACA TCATCGTTTT CAACATTCCA	480
CATCAATTTT TGCCCCGTAT CTGTAGCCAA TTGAAAGGTC ATGTTGATTC ACACGTCAGA	540
GCTATCTCCT GTCTAAAGGG TTTTGAAGTT GGTGCTAAAG GTGTCCAATT GCTATCCTCT	600
TACATCACTG AGGAACTAGG TATTCAATGT GGTGCTCTAT CTGGTGCTAA CATTGCCACC	660
GAAGTCGCTC AAGAACACTG GTCTGAAACA ACAGTTGCTT ACCACATTCC AAAGGATTTT	720

AGAGGCGAGG	GCAAGGACGT	CGACCATAAG	GTTCTAAAGG	CCTTGTTCCA	CAGACCTTAC	780
TTCCACGTTA	GTGTCATCGA	AGATGTTGCT	GGTATCTCCA	TCTGTGGTGC	TTTGAAGAAC	840
GTTGTTGCCT	TAGGTTGTGG	TTTCGTCGAA	GGTCTAGGCT	GGGGTAACAA	CGCTTCTGCT	900
GCCATCCAAA	GAGTCGGTTT	GGGTGAGATC	ATCAGATTCT	GTCAAATGTT	TTTCCCAGAA	960
TCTAGAGAAG	AAACATACTA	CCAAGAGTCT	GCTGGTGTTG	CTGATTTGAT	CACCACCTGC	1020
GCTGGTGGTA	GAAACGTCAA	GGTTGCTAGG	CTAATGGCTA	CTTCTGGTAA	GGACGCCTGG	1080
GAATGTGAAA	AGGAGTTGTT	GAATGGCCAA	TCCGCTCAAG	GTTTAATTAC	CTGCAAAGAA	1140
GTTACGAAT	GGTTGGAAAC	ATGTGGCTCT	GTCGAAGACT	TCCCATTATT	TGAAGCCGTA	1200
TACCAAATCG	TTTACAACAA	CTACCCAATG	AAGAACCTGC	CGGACATGAT	TGAAGAATTA	1260
GATCTACATG	AAGATTAGAT	TTATTGGAGA	AAGATAACAT	ATCATACTTC	CCCCACTTTT	1320
TTGAGGCTC	TTCTATATCA	TATTCATAAA	TTAGCATTAT	GTCATTTCTC	ATAACTACTT	1380

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2946 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: GPD2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATTCGAGC	CTGAAGTGCT	GATTACCTTC	AGGTAGACTT	CATCTTGACC	CATCAACCCC	60
AGCGTCAATC	CTGCAAATAC	ACCACCCAGC	AGCACTAGGA	TGATAGAGAT	AATATAGTAC	120
GTGGTAACGC	TTGCCTCATC	ACCTACGCTA	TGGCCGGAAT	CGGCAACATC	CCTAGAATTG	180
AGTACGTGTG	ATCCGGATAA	CAACGGCAGT	GAATATATCT	TCGGTATCGT	AAAGATGTGA	240
TATAAGATGA	TGTATACCCA	ATGAGGAGCG	CCTGATCGTG	ACCTAGACCT	TAGTGGCAAA	300
AACGACATAT	CTATTATAGT	GGGGAGAGTT	TCGTGCAAAT	AACAGACGCA	GCAGCAAGTA	360
ACTGTGACGA	TATCAACTCT	TTTTTTATTA	TGTAATAAGC	AAACAAGCAC	GAATGGGGAA	420
AGCCTATGTG	CAATCACCAA	GGTCGTCCCT	TTTTTCCCAT	TTGCTAATTT	AGAATTTAAA	480
GAAACCAAAA	GAATGAAGAA	AGAAAACAAA	TACTAGCCCT	AACCCTGACT	TCGTTTCTAT	540
GATAATACCC	TGCTTTAATG	AACGGTATGC	CCTAGGGTAT	ATCTCACTCT	GTACGTTACA	600

AACTCCGGTT	ATTTTATCGG	AACATCCGAG	CACCCGCGCC	TTCTCAACC	CAGGCACCGC	660
CCCAGGTAAC	CGTGCGGAT	GAGCTAATCC	TGAGCCATCA	CCCACCCAC	CCGTTGATGA	720
CAGCAATTCG	GGAGGGCGAA	AATAAACTG	GAGCAAGGAA	TTACCATCAC	CGTCACCATC	780
ACCATCATAT	CGCCTTAGCC	TCTAGCCATA	GCCATCATGC	AAGCGTGTAT	CTTCTAAGAT	840
TCAGTCATCA	TCATTACCGA	GTTTGTTTTC	CTTCACATGA	TGAAGAAGGT	TTGAGTATGC	900
TCGAAACAAT	AAGACGACGA	TGGCTCTGCC	ATTGGTTATA	TTACGCTTTT	GCGGCGAGGT	960
GCCGATGGGT	TGCTGAGGGG	AAGAGTGTTC	AGCTTACGGA	CCTATTGCCA	TTGTTATTCC	1020
GATTAATCTA	TTGTTACGCA	GCTCTTCTCT	ACCCTGTCAT	TCTAGTATTT	TTTTTTTTTT	1080
TTTTTGTTTT	TACTTTTTTT	TCTTCTTGCC	TTTTTTTCTT	GTTACTTTTT	TTCTAGTTTT	1140
TTTTTCCTTC	ACTAAGCTTT	TTCTTGATT	TATCCTTGGG	TTCTTCTTTC	TACTCCTTTA	1200
GATTTTTTTT	TTATATATTA	ATTTTTAAGT	TTATGTATTT	TGGTAGATTC	AATTCTCTTT	1260
CCCTTTCCTT	TTCTTCGCT	CCCCTTCCTT	ATCAATGCTT	GCTGTCAGAA	GATTAACAAG	1320
ATACACATTC	CTTAAGCGAA	CGCATCCGGT	GTTATATACT	CGTCGTGCAT	ATAAAATTTT	1380
GCCTTCAAGA	TCTACTTTCC	TAAGAAGATC	ATTATTACAA	ACACAACGTC	ACTCAAAGAT	1440
GACTGCTCAT	ACTAATATCA	AACAGCACAA	ACACTGTCAT	GAGGACCATC	CTATCAGAAG	1500
ATCGGACTCT	GCCGTGTCAA	TTGTACATTT	GAAACGTGCG	CCCTTCAAGG	TTACAGTGAT	1560
TGGTTCTGGT	AACTGGGGGA	CCACCATCGC	CAAAGTCATT	GCGGAAAACA	CAGAATTGCA	1620
TTCCCATATC	TTGAGCCAG	AGGTGAGAAT	GTGGGTTTTT	GATGAAAAGA	TCGGCGACGA	1680
AAATCTGACG	GATATCATAA	ATACAAGACA	CCAGAACGTT	AAATATCTAC	CCAATATTGA	1740
CCTGCCCCAT	AATCTAGTGG	CCGATCCTGA	TCTTTTACAC	TCCATCAAGG	GTGCTGACAT	1800
CCTTGTTTTT	AACATCCCTC	ATCAATTTTT	ACCAAACATA	GTCAAACAAT	TGCAAGGCCA	1860
CGTGGCCCCT	CATGTAAGGG	CCATCTCGTG	TCTAAAAGGG	TTGAGTTGG	GCTCCAAGGG	1920
TGTGCAATTG	CTATCCTCCT	ATGTTACTGA	TGAGTTAGGA	ATCCAATGTG	GCGCACTATC	1980
TGGTGCAAAC	TTGGCACCGG	AAGTGGCCAA	GGAGCATTGG	TCCGAAACCA	CCGTGGCTTA	2040
CCAACTACCA	AAGGATTATC	AAGGTGATGG	CAAGGATGTA	GATCATAAGA	TTTTGAAATT	2100
GCTGTTCCAC	AGACCTTACT	TCCACGTCAA	TGTCATCGAT	GATGTTGCTG	GTATATCCAT	2160
TGCCGGTGCC	TTGAAGAACG	TCGTGGCACT	TGCATGTGGT	TTCGTAGAAG	GTATGGGATG	2220
GGGTAACAAT	GCCTCCGCAG	CCATTCAAAG	GCTGGGTTTA	GGTGAAATTA	TCAAGTTCGG	2280

TAGAATGTTT TTCCCAGAAT CCAAAGTCGA GACCTACTAT CAAGAATCCG CTGGTGTTGC 2340  
 AGATCTGATC ACCACCTGCT CAGGCGGTAG AAACGTCAAG GTTGCCACAT ACATGGCCAA 2400  
 GACCGGTAAG TCAGCCTTGG AAGCAGAAAA GGAATTGCTT AACGGTCAAT CCGCCCAAGG 2460  
 GATAATCACA TGCAGAGAAG TTCACGAGTG GCTACAAACA TGTGAGTTGA CCCAAGAATT 2520  
 CCCAATTATT CGAGGCAGTC TACCAGATAG TCTACAACAA CGTCCGCATG GAAGACCTAC 2580  
 CGGAGATGAT TGAAGAGCTA GACATCGATG ACGAATAGAC ACTCTCCCCC CCCCTCCCCC 2640  
 TCTGATCTTT CCTGTTGCCT CTTTTTCCCC CAACCAATTT ATCATTATAC ACAAGTTCTA 2700  
 CAACTACTAC TAGTAACATT ACTACAGTTA TTATAATTTT CTATTCTCTT TTTCTTTAAG 2760  
 AATCTATCAT TAACGTTAAT TTCTATATAT ACATAACTAC CATTATACAC GCTATTATCG 2820  
 TTTACATATC ACATCACCGT TAATGAAAGA TACGACACCC TGTACACTAA CACAATTAAA 2880  
 TAATCGCCAT AACCTTTTCT GTTATCTATA GCCCTTAAAG CTGTTTCTTC GAGCTTTTCA 2940  
 CTGCAG 2946

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3178 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: GUT2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTGCAGAACT TCGTCTGCTC TGTGCCCATC CTCGCGGTTA GAAAGAAGCT GAATTGTTTC 60  
 ATGCGCAAGG GCATCAGCGA GTGACCAATA ATCACTGCAC TAATTCCTTT TTAGCAACAC 120  
 ATACTTATAT ACAGCACCAG ACCTTATGTC TTTTCTCTGC TCCGATACGT TATCCCACCC 180  
 AACTTTTATT TCAGTTTTGG CAGGGGAAAT TTCACAACCC CGCACGCTAA AAATCGTATT 240  
 TAAACTTAAA AGAGAACAGC CACAAATAGG GAACTTTGGT CTAAACGAAG GACTCTCCCT 300  
 CCCTTATCTT GACCGTGCTA TTGCCATCAC TGCTACAAGA CTAAATACGT ACTAATATAT 360  
 GTTTTCGGTA ACGAGAAGAA GAGCTGCCGG TGCAGCTGCT GCCATGGCCA CAGCCACGGG 420  
 GACGCTGTAC TGGATGACTA GCCAAGGTGA TAGGCCGTTA GTGCACAATG ACCCGAGCTA 480  
 CATGGTGCAA TTCCCCACCG CCGCTCCACC GGCAGGTCTC TAGACGAGAC CTGCTGGACC 540



GTCTGGACAA	GACGCATCAA	TTCGACGTGT	TGATCATCGG	TGGCGGGGCC	ACGGGGACAG	600
GATGTGCCCT	AGATGCTGCG	ACCAGGGGAC	TCAATGTGGC	CCTTGTTGAA	AAGGGGGATT	660
TTGCCTCGGG	AACGTCGTCC	AAATCTACCA	AGATGATTCA	CGGTGGGGTG	CGGTACTTAG	720
AGAAGGCCTT	CTGGGAGTTC	TCCAAGGCAC	AACTGGATCT	GGTCATCGAG	GCACTCAACG	780
AGCGTAAACA	TCTTATCAAC	ACTGCCCCCTC	ACCTGTGCAC	GGTGCTACCA	ATTCTGATCC	840
CCATCTACAG	CACCTGGCAG	GTCCCGTACA	TCTATATGGG	CTGTAAATTC	TACGATTTCT	900
TTGGCGGTTT	CCAAAACCTG	AAAAAATCAT	ACCTACTGTC	CAAATCCGCC	ACCGTGAGGA	960
AGGCTCCCAT	GCTTACCACA	GACAATTTAA	AGGCCTCGCT	TGTGTACCAT	GATGGGTCCT	1020
TTAACGACTC	GCGTTTGAAC	GCCACTTTAG	CCATCACGGG	TGTGGAGAAC	GGCGCTACCG	1080
TCTTGATCTA	TGTCGAGGTA	CAAAAATTGA	TCAAAGACCC	AACTTCTGGT	AAGGTTATCG	1140
GTGCCGAGGC	CCGGGACGTT	GAGACTAATG	AGCTTGTGAG	AATCAACGCT	AAATGTGTGG	1200
TCAATGCCAC	GGGCCCATAC	AGTGACGCCA	TTTTGCAAAT	GGACCGCAAC	CCATCCGGTC	1260
TGCCGGACTC	CCCCTAAAC	GACAACTCCA	AGATCAAGTC	GACTTTCAAT	CAAATCTCCG	1320
TCATGGACCC	GAAAATGGTC	ATCCCATCTA	TTGGCGTTCA	CATCGTATTG	CCCTCTTTTT	1380
ACTCCCCGAA	GGATATGGGT	TTGTTGGACG	TCAGAACCTC	TGATGGCAGA	GTGATGTTCT	1440
TTTTACCTTG	GCAGGGCAAA	GTCTTGGCCG	GCACCACAGA	CATCCCACTA	AAGCAAGTCC	1500
CAGAAAACCC	TATGCCTACA	GAGGCTGATA	TTCAAGATAT	CTTGAAAGAA	CTACAGCACT	1560
ATATCGAATT	CCCCGTGAAA	AGAGAAGACG	TGCTAAGTGC	ATGGGCTGGT	GTCAGACCTT	1620
TGGTCAGAGA	TCCACGTACA	ATCCCCGCAG	ACGGGAAGAA	GGGCTCTGCC	ACTCAGGGCG	1680
TGGTAAGATC	CCACTTCTTG	TTCACTTCGG	ATAATGGCCT	AATTACTATT	GCAGGTGGTA	1740
AATGGACTAC	TTACAGACAA	ATGGCTGAGG	AAACAGTCGA	CAAAGTTGTC	GAAGTTGGCG	1800
GATTCCACAA	CCTGAAACCT	TGTCACACAA	GAGATATTAA	GCTTGCTGGT	GCAGAAGAAT	1860
GGACGCAAAA	CTATGTGGCT	TTATTGGCTC	AAAACCTACCA	TTTATCATCA	AAAATGTCCA	1920
ACTACTTGGT	TCAAACTAC	GGAACCCGTT	CCTCTATCAT	TTGCGAATTT	TTCAAAGAAT	1980
CCATGGAAAA	TAAACTGCCT	TTGTCTTAG	CCGACAAGGA	AAATAACGTA	ATCTACTCTA	2040
GCGAGGAGAA	CAACTTGGTC	AATTTTGATA	CTTTCAGATA	TCCATTACAA	ATCGGTGAGT	2100
TAAAGTATTC	CATGCAGTAC	GAATATTGTA	GAACTCCCTT	GGACTTCCTT	TTAAGAAGAA	2160
CAAGATTTCG	CTTCTTGGAC	GCCAAGGAAG	CTTTGAATGC	CGTGCATGCC	ACCGTCAAAG	2220
TTATGGGTGA	TGAGTTCAAT	TGGTCGGAGA	AAAAGAGGCA	GTGGGAACCT	GAAAAAACTG	2280

TGAACTTCAT CCAAGGACGT TTCGGTGTCT AAATCGATCA TGATAGTTAA GGGTGACAAA	2340
GATAACATTC ACAAGAGTAA TAATAATGGT AATGATGATA ATAATAATAA TGATAGTAAT	2400
AACAATAATA ATAATGGTGG TAATGGCAAT GAAATCGCTA TTATTACCTA TTTTCCTTAA	2460
TGGAAGAGTT AAAGTAACT AAAAAAACTA CAAAAATATA TGAAGAAAAA AAAAAAAGA	2520
GGTAATAGAC TCTACTACTA CAATTGATCT TCAAATTATG ACCTTCCTAG TGTTTATATT	2580
CTATTTCCAA TACATAATAT AATCTATATA ATCATTGCTG GTAGACTTCC GTTTTAATAT	2640
CGTTTTAATT ATCCCCTTTA TCTCTAGTCT AGTTTTATCA TAAAATATAG AAACACTAAA	2700
TAATATTCTT CAAACGGTCC TGGTGCATAC GCAATACATA TTTATGGTGC AAAAAAAAAA	2760
ATGGAAAATT TTGCTAGTCA TAAACCCTTT CATAAAACAA TACGTAGACA TCGCTACTTG	2820
AAATTTTCAA GTTTTTATCA GATCCATGTT TCCTATCTGC CTTGACAACC TCATCGTCGA	2880
AATAGTACCA TTTAGAACGC CCAATATTCA CATTGTGTTC AAGGTCTTTA TTCACCAGTG	2940
ACGTGTAATG GCCATGATTA ATGTGCCTGT ATGGTTAACC ACTCAAATA GCTTATATTT	3000
CATAGTGTCA TTGTTTTTCA ATATAATGTT TAGTATCAAT GGATATGTTA CGACGGTGTT	3060
ATTTTTCTTG GTCAAATCGT AATAAAATCT CGATAAATGG ATGACTAAGA TTTTGGTAA	3120
AGTTACAAA TTTATCGTTT TCACTGTTGT CAATTTTTTG TTCTTGTAAT CACTCGAG	3178

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 816 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: GPP1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAAACGTT TCAATGTTTT AAAATATATC AGAACAACAA AAGCAAATAT ACAAACCATC	60
GCAATGCCTT TGACCACAAA ACCTTTATCT TTGAAAATCA ACGCCGCTCT ATTCGATGTT	120
GACGGTACCA TCATCATCTC TCAACCAGCC ATTGCTGCTT TCTGGAGAGA TTTCGGTAAA	180
GACAAGCCTT ACTTCGATGC CGAACACGTT ATTCACATCT CTCACGGTTG GAGAACTTAC	240
GATGCCATTG CCAAGTTCGC TCCAGACTTT GCTGATGAAG AATACGTTAA CAAGCTAGAA	300
GGTGAAATCC CAGAAAAGTA CGGTGAACAC TCCATCGAAG TTCCAGGTGC TGTCAAGTTG	360

TGTAATGCTT TGAACGCCTT GCCAAAAGGAA AAATGGGCTG TCGCCACCTC TGGTACCCGT	420
GACATGGCCA AGAAATGGTT CGACATTTTG AAGATCAAGA GACCAGAATA CTTTCATCACC	480
GCCAATGATG TCAAGCAAGG TAAGCCTCAC CCAGAACCAT ACTTAAAGGG TAGAAACGGT	540
TTGGGTTTCC CAATTAATGA ACAAGACCCA TCCAAATCTA AGGTTGTTGT CTTTGAAGAC	600
GCACCAGCTG GTATTGCTGC TGGTAAGGCT GCTGGCTGTA AAATCGTTGG TATTGCTACC	660
ACTTTCGATT TGGACTTCTT GAAGGAAAAAG GGTGTGACA TCATTGTCAA GAACCACGAA	720
TCTATCAGAG TCGGTGAATA CAACGCTGAA ACCGATGAAG TCGAATTGAT CTTTGATGAC	780
TACTTATACG CTAAGGATGA CTTGTTGAAA TGGTAA	816

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 753 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: GPP2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGGGATTGA CTACTAAACC TCTATCTTTG AAAGTTAACG CCGCTTTGTT CGACGTCGAC	60
GGTACCATTA TCATCTCTCA ACCAGCCATT GCTGCATTCT GGAGGGATTT CGGTAAGGAC	120
AAACCTTATT TCGATGCTGA ACACGTTATC CAAGTCTCGC ATGGTTGGAG AACGTTTGAT	180
GCCATTGCTA AGTTCGCTCC AGACTTTGCC AATGAAGAGT ATGTTAACAA ATTAGAAGCT	240
GAAATTCCGG TCAAGTACGG TGAAAAATCC ATTGAAGTCC CAGGTGCAGT TAAGCTGTGC	300
AACGCTTTGA ACGCTCTACC AAAAGAGAAA TGGGCTGTGG CAACTTCCGG TACCCGTGAT	360
ATGGCACAAA AATGGTTCGA GCATCTGGGA ATCAGGAGAC CAAAGTACTT CATTACCGCT	420
AATGATGTCA AACAGGGTAA GCCTCATCCA GAACCATATC TGAAGGGCAG GAATGGCTTA	480
GGATATCCGA TCAATGAGCA AGACCCTTCC AAATCTAAGG TAGTAGTATT TGAAGACGCT	540
CCAGCAGGTA TTGCCGCCGG AAAAGCCGCC GGTGTGAAGA TCATTGGTAT TGCCACTACT	600
TTCGACTTGG ACTTCCTAAA GGAAAAAGGC TGTGACATCA TTGTCAAAAA CCACGAATCC	660
ATCAGAGTTG GCGGCTACAA TGCCGAAACA GACGAAGTTG AATTCATTTT TGACGACTAC	720
TTATATGCTA AGGACGATCT GTTGAAATGG TAA	753

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: GUT1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGTATTGGCC ACGATAACCA CCCTTTGTAT ACTGTTTTTTG TTTTTCACAT GGTAAATAAC	60
GACTTTTATT AAACAACGTA TGTA AAAACA TAACAAGAAT CTACCCATAC AGGCCATTTC	120
GTAATTCTTC TCTTCTAATT GGAGTAA AAC CATCAATTAA AGGGTGTGGA GTAGCATAGT	180
GAGGGGCTGA CTGCATTGAC AAAAAAATTG AAAAAAAAAA AGGAAAAGGA AAGGAAAAAA	240
AGACAGCCAA GACTTTTAGA ACGGATAAGG TGTAATAAAA TGTGGGGGGA TGCCTGTTCT	300
CGAACCATAT AAAATATACC ATGTGGTTTG AGTTGTGGCC GGA ACTATAC AAATAGTTAT	360
ATGTTTCCCT CTCTCTTCCG ACTTG TAGTA TTCTCCAAAC GTTACATATT CCGATCAAGC	420
CAGCGCCTTT AACTAGTTT AAAACAAGAA CAGAGCCGTA TGTCCAAAAT AATGGAAGAT	480
TTACGAAGTG ACTACGTCCC GCTTATCGCC AGTATTGATG TAGGAACGAC CTCATCCAGA	540
TGCATTCTGT TCAACAGATG GGGCCAGGAC GTTTC AAAAC ACCAAATTGA ATATTCAACT	600
TCAGCATCGA AGGGCAAGAT TGGGGTGTCT GGCCTAAGGA GACCCTCTAC AGCCCCAGCT	660
CGTGAAACAC CAAACGCCGG TGACATCAAA ACCAGCGGAA AGCCCATCTT TTCTGCAGAA	720
GGCTATGCCA TTCAAGAAAC CAAATTCCTA AAAATCGAGG AATTGGACTT GGACTTCCAT	780
AACGAACCCA CGTTGAAGTT CCCC AAACCG GGT TGGGTTG AGTGCCATCC GCAGAAATTA	840
CTGGTGAACG TCGTCCAATG CCTTGCCTCA AGTTTGCTCT CTCTGCAGAC TATCAACAGC	900
GAACGTGTAG CAAACGGTCT CCCACCTTAC AAGGTAATAT GCATGGGTAT AGCAAACATG	960
AGAGAAACCA CAATTCTGTG GTCCCGCCGC ACAGGAAAAC CAATTGTTAA CTACGGTATT	1020
GTTTGGAACG ACACCAGAAC GATCAAAATC GTTAGAGACA AATGGCAAAA CACTAGCGTC	1080
GATAGGCAAC TGCAGCTTAG ACAGAAGACT GGATTGCCAT TGCTCTCCAC GTATTTCTCC	1140
TGTTCCAAGC TGCGCTGGTT CCTCGACAAT GAGCCTCTGT GTACCAAGGC GTATGAGGAG	1200
AACGACCTGA TGTTCCGCAC TGTGGACACA TGGCTGATTT ACCAATTAAC TAAACAAAAG	1260

GCGTTCGTTT	CTGACGTAAC	CAACGCTTCC	AGAACTGGAT	TTATGAACCT	CTCCACTTTA	1320
AAGTACGACA	ACGAGTTGCT	GGAATTTTGG	GGTATTGACA	AGAACCTGAT	TCACATGCCC	1380
GAAATTGTGT	CCTCATCTCA	ATACTACGGT	GACTTTGGCA	TTCCTGATTG	GATAATGGAA	1440
AAGCTACACG	ATTCGCCAAA	AACAGTACTG	CGAGATCTAG	TCAAGAGAAA	CCTGCCCATA	1500
CAGGGCTGTC	TGGGCGACCA	AAGCGCATCC	ATGGTGGGGC	AACTCGCTTA	CAAACCCGGT	1560
GCTGCAAAAT	GTACTIONTATGG	TACCGGTTGC	TTTTTACTGT	ACAATACGGG	GACCAAAAAA	1620
TTGATCTCCC	AACATGGCGC	ACTGACGACT	CTAGCATTTT	GGTCCCACA	TTTGCAAGAG	1680
TACGGTGGCC	AAAAACCAGA	ATTGAGCAAG	CCACATTTTG	CATTAGAGGG	TTCCGTCGCT	1740
GTGGCTGGTG	CTGTGGTCCA	ATGGCTACGT	GATAATTTAC	GATTGATCGA	TAAATCAGAG	1800
GATGTCGGAC	CGATTGCATC	TACGGTTCCT	GATTCTGGTG	GCGTAGTTTT	CGTCCCCGCA	1860
TTTAGTGGCC	TATTCGCTCC	CTATTGGGAC	CCAGATGCCA	GAGCCACCAT	AATGGGGATG	1920
TCTCAATTCA	CTACTGCCTC	CCACATCGCC	AGAGCTGCCG	TGGAAGGTGT	TTGCTTTCAA	1980
GCCAGGGCTA	TCTTGAAGGC	AATGAGTTCT	GACGCGTTTG	GTGAAGGTTC	CAAAGACAGG	2040
GACTTTTTTAG	AGGAAATTTT	CGACGTCACA	TATGAAAAGT	CGCCCCTGTC	GGTTCTGGCA	2100
GTGGATGGCG	GGATGTGAG	GTCTAATGAA	GTCATGCAAA	TTCAAGCCGA	TATCCTAGGT	2160
CCCTGTGTCA	AAGTCAGAAG	GTCTCCGACA	GCGGAATGTA	CCGCATTGGG	GGCAGCCATT	2220
GCAGCCAATA	TGGCTTTCAA	GGATGTGAAC	GAGCGCCCAT	TATGGAAGGA	CCTACACGAT	2280
GTTAAGAAAT	GGGTCTTTTA	CAATGGAATG	GAGAAAAACG	AACAAATATC	ACCAGAGGCT	2340
CATCCAAACC	TTAAGATATT	CAGAAGTGAA	TCCGACGATG	CTGAAAGGAG	AAAGCATTGG	2400
AAGTATTGGG	AAGTTGCCGT	GGAAAGATCC	AAAGGTTGGC	TGAAGGACAT	AGAAGGTGAA	2460
CACGAACAGG	TTCTAGAAAA	CTTCCAATAA	CAACATAAAT	AATTTCTATT	AACAATGTAA	2520

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: GPD1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Ser	Ala	Ala	Ala	Asp	Arg	Leu	Asn	Leu	Thr	Ser	Gly	His	Leu	Asn	1	5	10	15
Ala	Gly	Arg	Lys	Arg	Ser	Ser	Ser	Ser	Val	Ser	Leu	Lys	Ala	Ala	Glu	20	25	30	
Lys	Pro	Phe	Lys	Val	Thr	Val	Ile	Gly	Ser	Gly	Asn	Trp	Gly	Thr	Thr	35	40	45	
Ile	Ala	Lys	Val	Val	Ala	Glu	Asn	Cys	Lys	Gly	Tyr	Pro	Glu	Val	Phe	50	55	60	
Ala	Pro	Ile	Val	Gln	Met	Trp	Val	Phe	Glu	Glu	Glu	Ile	Asn	Gly	Glu	65	70	75	80
Lys	Leu	Thr	Glu	Ile	Ile	Asn	Thr	Arg	His	Gln	Asn	Val	Lys	Tyr	Leu	85	90	95	
Pro	Gly	Ile	Thr	Leu	Pro	Asp	Asn	Leu	Val	Ala	Asn	Pro	Asp	Leu	Ile	100	105	110	
Asp	Ser	Val	Lys	Asp	Val	Asp	Ile	Ile	Val	Phe	Asn	Ile	Pro	His	Gln	115	120	125	
Phe	Leu	Pro	Arg	Ile	Cys	Ser	Gln	Leu	Lys	Gly	His	Val	Asp	Ser	His	130	135	140	
Val	Arg	Ala	Ile	Ser	Cys	Leu	Lys	Gly	Phe	Glu	Val	Gly	Ala	Lys	Gly	145	150	155	160
Val	Gln	Leu	Leu	Ser	Ser	Tyr	Ile	Thr	Glu	Glu	Leu	Gly	Ile	Gln	Cys	165	170	175	
Gly	Ala	Leu	Ser	Gly	Ala	Asn	Ile	Ala	Thr	Glu	Val	Ala	Gln	Glu	His	180	185	190	
Trp	Ser	Glu	Thr	Thr	Val	Ala	Tyr	His	Ile	Pro	Lys	Asp	Phe	Arg	Gly	195	200	205	
Glu	Gly	Lys	Asp	Val	Asp	His	Lys	Val	Leu	Lys	Ala	Leu	Phe	His	Arg	210	215	220	
Pro	Tyr	Phe	His	Val	Ser	Val	Ile	Glu	Asp	Val	Ala	Gly	Ile	Ser	Ile	225	230	235	240
Cys	Gly	Ala	Leu	Lys	Asn	Val	Val	Ala	Leu	Gly	Cys	Gly	Phe	Val	Glu	245	250	255	
Gly	Leu	Gly	Trp	Gly	Asn	Asn	Ala	Ser	Ala	Ala	Ile	Gln	Arg	Val	Gly	260	265	270	
Leu	Gly	Glu	Ile	Ile	Arg	Phe	Gly	Gln	Met	Phe	Phe	Pro	Glu	Ser	Arg	275	280	285	
Glu	Glu	Thr	Tyr	Tyr	Gln	Glu	Ser	Ala	Gly	Val	Ala	Asp	Leu	Ile	Thr	290	295	300	

Thr Cys Ala Gly Gly Arg Asn Val Lys Val Ala Arg Leu Met Ala Thr  
 305 310 315 320  
 Ser Gly Lys Asp Ala Trp Glu Cys Glu Lys Glu Leu Leu Asn Gly Gln  
 325 330 335  
 Ser Ala Gln Gly Leu Ile Thr Cys Lys Glu Val His Glu Trp Leu Glu  
 340 345 350  
 Thr Cys Gly Ser Val Glu Asp Phe Pro Leu Phe Glu Ala Val Tyr Gln  
 355 360 365  
 Ile Val Tyr Asn Asn Tyr Pro Met Lys Asn Leu Pro Asp Met Ile Glu  
 370 375 380  
 Glu Leu Asp Leu His Glu Asp  
 385 390

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 384 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: GPD2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Thr Ala His Thr Asn Ile Lys Gln His Lys His Cys His Glu Asp  
 1 5 10 15  
 His Pro Ile Arg Arg Ser Asp Ser Ala Val Ser Ile Val His Leu Lys  
 20 25 30  
 Arg Ala Pro Phe Lys Val Thr Val Ile Gly Ser Gly Asn Trp Gly Thr  
 35 40 45  
 Thr Ile Ala Lys Val Ile Ala Glu Asn Thr Glu Leu His Ser His Ile  
 50 55 60  
 Phe Glu Pro Glu Val Arg Met Trp Val Phe Asp Glu Lys Ile Gly Asp  
 65 70 75 80  
 Glu Asn Leu Thr Asp Ile Ile Asn Thr Arg His Gln Asn Val Lys Tyr  
 85 90 95  
 Leu Pro Asn Ile Asp Leu Pro His Asn Leu Val Ala Asp Pro Asp Leu  
 100 105 110  
 Leu His Ser Ile Lys Gly Ala Asp Ile Leu Val Phe Asn Ile Pro His  
 115 120 125

Gln	Phe	Leu	Pro	Asn	Ile	Val	Lys	Gln	Leu	Gln	Gly	His	Val	Ala	Pro	
130						135					140					
His	Val	Arg	Ala	Ile	Ser	Cys	Leu	Lys	Gly	Phe	Glu	Leu	Gly	Ser	Lys	
145					150					155					160	
Gly	Val	Gln	Leu	Leu	Ser	Ser	Tyr	Val	Thr	Asp	Glu	Leu	Gly	Ile	Gln	
				165					170					175		
Cys	Gly	Ala	Leu	Ser	Gly	Ala	Asn	Leu	Ala	Pro	Glu	Val	Ala	Lys	Glu	
			180					185						190		
His	Trp	Ser	Glu	Thr	Thr	Val	Ala	Tyr	Gln	Leu	Pro	Lys	Asp	Tyr	Gln	
		195					200						205			
Gly	Asp	Gly	Lys	Asp	Val	Asp	His	Lys	Ile	Leu	Lys	Leu	Leu	Phe	His	
	210					215					220					
Arg	Pro	Tyr	Phe	His	Val	Asn	Val	Ile	Asp	Asp	Val	Ala	Gly	Ile	Ser	
225					230					235					240	
Ile	Ala	Gly	Ala	Leu	Lys	Asn	Val	Val	Ala	Leu	Ala	Cys	Gly	Phe	Val	
				245					250					255		
Glu	Gly	Met	Gly	Trp	Gly	Asn	Asn	Ala	Ser	Ala	Ala	Ile	Gln	Arg	Leu	
			260					265						270		
Gly	Leu	Gly	Glu	Ile	Ile	Lys	Phe	Gly	Arg	Met	Phe	Phe	Pro	Glu	Ser	
		275					280					285				
Lys	Val	Glu	Thr	Tyr	Tyr	Gln	Glu	Ser	Ala	Gly	Val	Ala	Asp	Leu	Ile	
	290					295						300				
Thr	Thr	Cys	Ser	Gly	Gly	Arg	Asn	Val	Lys	Val	Ala	Thr	Tyr	Met	Ala	
305					310						315				320	
Lys	Thr	Gly	Lys	Ser	Ala	Leu	Glu	Ala	Glu	Lys	Glu	Leu	Leu	Asn	Gly	
				325					330					335		
Gln	Ser	Ala	Gln	Gly	Ile	Ile	Thr	Cys	Arg	Glu	Val	His	Glu	Trp	Leu	
			340					345					350			
Gln	Thr	Cys	Glu	Leu	Thr	Gln	Glu	Phe	Pro	Ile	Ile	Arg	Gly	Ser	Leu	
		355					360					365				
Pro	Asp	Ser	Leu	Gln	Gln	Arg	Pro	His	Gly	Arg	Pro	Thr	Gly	Asp	Asp	
	370					375						380				

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 614 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown



(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: GUT2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Thr	Arg	Ala	Thr	Trp	Cys	Asn	Ser	Pro	Pro	Pro	Leu	His	Arg	Gln	
1				5					10					15		
Val	Ser	Arg	Arg	Asp	Leu	Leu	Asp	Arg	Leu	Asp	Lys	Thr	His	Gln	Phe	
			20					25					30			
Asp	Val	Leu	Ile	Ile	Gly	Gly	Gly	Ala	Thr	Gly	Thr	Gly	Cys	Ala	Leu	
		35					40					45				
Asp	Ala	Ala	Thr	Arg	Gly	Leu	Asn	Val	Ala	Leu	Val	Glu	Lys	Gly	Asp	
	50					55					60					
Phe	Ala	Ser	Gly	Thr	Ser	Ser	Lys	Ser	Thr	Lys	Met	Ile	His	Gly	Gly	
65					70					75					80	
Val	Arg	Tyr	Leu	Glu	Lys	Ala	Phe	Trp	Glu	Phe	Ser	Lys	Ala	Gln	Leu	
			85						90					95		
Asp	Leu	Val	Ile	Glu	Ala	Leu	Asn	Glu	Arg	Lys	His	Leu	Ile	Asn	Thr	
		100						105					110			
Ala	Pro	His	Leu	Cys	Thr	Val	Leu	Pro	Ile	Leu	Ile	Pro	Ile	Tyr	Ser	
		115					120					125				
Thr	Trp	Gln	Val	Pro	Tyr	Ile	Tyr	Met	Gly	Cys	Lys	Phe	Tyr	Asp	Phe	
	130					135					140					
Phe	Gly	Gly	Ser	Gln	Asn	Leu	Lys	Lys	Ser	Tyr	Leu	Leu	Ser	Lys	Ser	
145					150					155					160	
Ala	Thr	Val	Glu	Lys	Ala	Pro	Met	Leu	Thr	Thr	Asp	Asn	Leu	Lys	Ala	
			165						170					175		
Ser	Leu	Val	Tyr	His	Asp	Gly	Ser	Phe	Asn	Asp	Ser	Arg	Leu	Asn	Ala	
		180						185					190			
Thr	Leu	Ala	Ile	Thr	Gly	Val	Glu	Asn	Gly	Ala	Thr	Val	Leu	Ile	Tyr	
		195					200					205				
Val	Glu	Val	Gln	Lys	Leu	Ile	Lys	Asp	Pro	Thr	Ser	Gly	Lys	Val	Ile	
	210					215					220					
Gly	Ala	Glu	Ala	Arg	Asp	Val	Glu	Thr	Asn	Glu	Leu	Val	Arg	Ile	Asn	
225					230					235					240	
Ala	Lys	Cys	Val	Val	Asn	Ala	Thr	Gly	Pro	Tyr	Ser	Asp	Ala	Ile	Leu	
			245						250					255		
Gln	Met	Asp	Arg	Asn	Pro	Ser	Gly	Leu	Pro	Asp	Ser	Pro	Leu	Asn	Asp	
		260						265					270			

Asn	Ser	Lys	Ile	Lys	Ser	Thr	Phe	Asn	Gln	Ile	Ser	Val	Met	Asp	Pro	
		275					280					285				
Lys	Met	Val	Ile	Pro	Ser	Ile	Gly	Val	His	Ile	Val	Leu	Pro	Ser	Phe	
	290					295					300					
Tyr	Ser	Pro	Lys	Asp	Met	Gly	Leu	Leu	Asp	Val	Arg	Thr	Ser	Asp	Gly	
305					310					315					320	
Arg	Val	Met	Phe	Phe	Leu	Pro	Trp	Gln	Gly	Lys	Val	Leu	Ala	Gly	Thr	
				325					330					335		
Thr	Asp	Ile	Pro	Leu	Lys	Gln	Val	Pro	Glu	Asn	Pro	Met	Pro	Thr	Glu	
			340					345					350			
Ala	Asp	Ile	Gln	Asp	Ile	Leu	Lys	Glu	Leu	Gln	His	Tyr	Ile	Glu	Phe	
		355					360					365				
Pro	Val	Lys	Arg	Glu	Asp	Val	Leu	Ser	Ala	Trp	Ala	Gly	Val	Arg	Pro	
	370					375					380					
Leu	Val	Arg	Asp	Pro	Arg	Thr	Ile	Pro	Ala	Asp	Gly	Lys	Lys	Gly	Ser	
385					390					395					400	
Ala	Thr	Gln	Gly	Val	Val	Arg	Ser	His	Phe	Leu	Phe	Thr	Ser	Asp	Asn	
				405					410					415		
Gly	Leu	Ile	Thr	Ile	Ala	Gly	Gly	Lys	Trp	Thr	Thr	Tyr	Arg	Gln	Met	
		420						425					430			
Ala	Glu	Glu	Thr	Val	Asp	Lys	Val	Val	Glu	Val	Gly	Gly	Phe	His	Asn	
	435					440						445				
Leu	Lys	Pro	Cys	His	Thr	Arg	Asp	Ile	Lys	Leu	Ala	Gly	Ala	Glu	Glu	
	450					455				460						
Trp	Thr	Gln	Asn	Tyr	Val	Ala	Leu	Leu	Ala	Gln	Asn	Tyr	His	Leu	Ser	
465					470					475				480		
Ser	Lys	Met	Ser	Asn	Tyr	Leu	Val	Gln	Asn	Tyr	Gly	Thr	Arg	Ser	Ser	
				485					490					495		
Ile	Ile	Cys	Glu	Phe	Phe	Lys	Glu	Ser	Met	Glu	Asn	Lys	Leu	Pro	Leu	
			500					505					510			
Ser	Leu	Ala	Asp	Lys	Glu	Asn	Asn	Val	Ile	Tyr	Ser	Ser	Glu	Glu	Asn	
		515					520					525				
Asn	Leu	Val	Asn	Phe	Asp	Thr	Phe	Arg	Tyr	Pro	Phe	Thr	Ile	Gly	Glu	
		530				535					540					
Leu	Lys	Tyr	Ser	Met	Gln	Tyr	Glu	Tyr	Cys	Arg	Thr	Pro	Leu	Asp	Phe	
545					550				555					560		
Leu	Leu	Arg	Arg	Thr	Arg	Phe	Ala	Phe	Leu	Asp	Ala	Lys	Glu	Ala	Leu	
				565					570				575			

Asn Ala Val His Ala Thr Val Lys Val Met Gly Asp Glu Phe Asn Trp  
580 585 590

Ser Glu Lys Lys Arg Gln Trp Glu Leu Glu Lys Thr Val Asn Phe Ile  
595 600 605

Gln Gly Arg Phe Gly Val  
610

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: GPSA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Asn Gln Arg Asn Ala Ser Met Thr Val Ile Gly Ala Gly Ser Tyr  
1 5 10 15

Gly Thr Ala Leu Ala Ile Thr Leu Ala Arg Asn Gly His Glu Val Val  
20 25 30

Leu Trp Gly His Asp Pro Glu His Ile Ala Thr Leu Glu Arg Asp Arg  
35 40 45

Cys Asn Ala Ala Phe Leu Pro Asp Val Pro Phe Pro Asp Thr Leu His  
50 55 60

Leu Glu Ser Asp Leu Ala Thr Ala Leu Ala Ala Ser Arg Asn Ile Leu  
65 70 75 80

Val Val Val Pro Ser His Val Phe Gly Glu Val Leu Arg Gln Ile Lys  
85 90 95

Pro Leu Met Arg Pro Asp Ala Arg Leu Val Trp Ala Thr Lys Gly Leu  
100 105 110

Glu Ala Glu Thr Gly Arg Leu Leu Gln Asp Val Ala Arg Glu Ala Leu  
115 120 125

Gly Asp Gln Ile Pro Leu Ala Val Ile Ser Gly Pro Thr Phe Ala Lys  
130 135 140

Glu Leu Ala Ala Gly Leu Pro Thr Ala Ile Ser Leu Ala Ser Thr Asp  
145 150 155 160

Gln Thr Phe Ala Asp Asp Leu Gln Gln Leu Leu His Cys Gly Lys Ser  
165 170 175

Phe Arg Val Tyr Ser Asn Pro Asp Phe Ile Gly Val Gln Leu Gly Gly  
180 185 190  
Ala Val Lys Asn Val Ile Ala Ile Gly Ala Gly Met Ser Asp Gly Ile  
195 200 205  
Gly Phe Gly Ala Asn Ala Arg Thr Ala Leu Ile Thr Arg Gly Leu Ala  
210 215 220  
Glu Met Ser Arg Leu Gly Ala Ala Leu Gly Ala Asp Pro Ala Thr Phe  
225 230 235 240  
Met Gly Met Ala Gly Leu Gly Asp Leu Val Leu Thr Cys Thr Asp Asn  
245 250 255  
Gln Ser Arg Asn Arg Arg Phe Gly Met Met Leu Gly Gln Gly Met Asp  
260 265 270  
Val Gln Ser Ala Gln Glu Lys Ile Gly Gln Val Val Glu Gly Tyr Arg  
275 280 285  
Asn Thr Lys Glu Val Arg Glu Leu Ala His Arg Phe Gly Val Glu Met  
290 295 300  
Pro Ile Thr Glu Glu Ile Tyr Gln Val Leu Tyr Cys Gly Lys Asn Ala  
305 310 315 320  
Arg Glu Ala Ala Leu Thr Leu Leu Gly Arg Ala Arg Lys Asp Glu Arg  
325 330 335  
Ser Ser His

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: GLPD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Glu Thr Lys Asp Leu Ile Val Ile Gly Gly Gly Ile Asn Gly Ala  
1 5 10 15  
Gly Ile Ala Ala Asp Ala Ala Gly Arg Gly Leu Ser Val Leu Met Leu  
20 25 30  
Glu Ala Gln Asp Leu Ala Cys Ala Thr Ser Ser Ala Ser Ser Lys Leu  
35 40 45

Ile His Gly Gly Leu Arg Tyr Leu Glu His Tyr Glu Phe Arg Leu Val  
 50 55 60

Ser Glu Ala Leu Ala Glu Arg Glu Val Leu Leu Lys Met Ala Pro His  
 65 70 75 80

Ile Ala Phe Pro Met Arg Phe Arg Leu Pro His Arg Pro His Leu Arg  
 85 90 95

Pro Ala Trp Met Ile Arg Ile Gly Leu Phe Met Tyr Asp His Leu Gly  
 100 105 110

Lys Arg Thr Ser Leu Pro Gly Ser Thr Gly Leu Arg Phe Gly Ala Asn  
 115 120 125

Ser Val Leu Lys Pro Glu Ile Lys Arg Gly Phe Glu Tyr Ser Asp Cys  
 130 135 140

Trp Val Asp Asp Ala Arg Leu Val Leu Ala Asn Ala Gln Met Val Val  
 145 150 155 160

Arg Lys Gly Gly Glu Val Leu Thr Arg Thr Arg Ala Thr Ser Ala Arg  
 165 170 175

Arg Glu Asn Gly Leu Trp Ile Val Glu Ala Glu Asp Ile Asp Thr Gly  
 180 185 190

Lys Lys Tyr Ser Trp Gln Ala Arg Gly Leu Val Asn Ala Thr Gly Pro  
 195 200 205

Trp Val Lys Gln Phe Phe Asp Asp Gly Met His Leu Pro Ser Pro Tyr  
 210 215 220

Gly Ile Arg Leu Ile Lys Gly Ser His Ile Val Val Pro Arg Val His  
 225 230 235 240

Thr Gln Lys Gln Ala Tyr Ile Leu Gln Asn Glu Asp Lys Arg Ile Val  
 245 250 255

Phe Val Ile Pro Trp Met Asp Glu Phe Ser Ile Ile Gly Thr Thr Asp  
 260 265 270

Val Glu Tyr Lys Gly Asp Pro Lys Ala Val Lys Ile Glu Glu Ser Glu  
 275 280 285

Ile Asn Tyr Leu Leu Asn Val Tyr Asn Thr His Phe Lys Lys Gln Leu  
 290 295 300

Ser Arg Asp Asp Ile Val Trp Thr Tyr Ser Gly Val Arg Pro Leu Cys  
 305 310 315 320

Asp Asp Glu Ser Asp Ser Pro Gln Ala Ile Thr Arg Asp Tyr Thr Leu  
 325 330 335

Asp Ile His Asp Glu Asn Gly Lys Ala Pro Leu Leu Ser Val Phe Gly  
 340 345 350

Gly Lys Leu Thr Thr Tyr Arg Lys Leu Ala Glu His Ala Leu Glu Lys  
 355 360 365  
 Leu Thr Pro Tyr Tyr Gln Gly Ile Gly Pro Ala Trp Thr Lys Glu Ser  
 370 375 380  
 Val Leu Pro Gly Gly Ala Ile Glu Gly Asp Arg Asp Asp Tyr Ala Ala  
 385 390 395 400  
 Arg Leu Arg Arg Arg Tyr Pro Phe Leu Thr Glu Ser Leu Ala Arg His  
 405 410 415  
 Tyr Ala Arg Thr Tyr Gly Ser Asn Ser Glu Leu Leu Leu Gly Asn Ala  
 420 425 430  
 Gly Thr Val Ser Asp Leu Gly Glu Asp Phe Gly His Glu Phe Tyr Glu  
 435 440 445  
 Ala Glu Leu Lys Tyr Leu Val Asp His Glu Trp Val Arg Arg Ala Asp  
 450 455 460  
 Asp Ala Leu Trp Arg Arg Thr Lys Gln Gly Met Trp Leu Asn Ala Asp  
 465 470 475 480  
 Gln Gln Ser Arg Val Ser Gln Trp Leu Val Glu Tyr Thr Gln Gln Arg  
 485 490 495  
 Leu Ser Leu Ala Ser  
 500

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 542 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: GLPABC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Lys Thr Arg Asp Ser Gln Ser Ser Asp Val Ile Ile Ile Gly Gly  
 1 5 10 15  
 Gly Ala Thr Gly Ala Gly Ile Ala Arg Asp Cys Ala Leu Arg Gly Leu  
 20 25 30  
 Arg Val Ile Leu Val Glu Arg His Asp Ile Ala Thr Gly Ala Thr Gly  
 35 40 45  
 Arg Asn His Gly Leu Leu His Ser Gly Ala Arg Tyr Ala Val Thr Asp  
 50 55 60

Ala	Glu	Ser	Ala	Arg	Glu	Cys	Ile	Ser	Glu	Asn	Gln	Ile	Leu	Lys	Arg	
65					70					75					80	
Ile	Ala	Arg	His	Cys	Val	Glu	Pro	Thr	Asn	Gly	Leu	Phe	Ile	Thr	Leu	
			85						90					95		
Pro	Glu	Asp	Asp	Leu	Ser	Phe	Gln	Ala	Thr	Phe	Ile	Arg	Ala	Cys	Glu	
		100						105					110			
Glu	Ala	Gly	Ile	Ser	Ala	Glu	Ala	Ile	Asp	Pro	Gln	Gln	Ala	Arg	Ile	
		115					120					125				
Ile	Glu	Pro	Ala	Val	Asn	Pro	Ala	Leu	Ile	Gly	Ala	Val	Lys	Val	Pro	
	130					135					140					
Asp	Gly	Thr	Val	Asp	Pro	Phe	Arg	Leu	Thr	Ala	Ala	Asn	Met	Leu	Asp	
145					150					155					160	
Ala	Lys	Glu	His	Gly	Ala	Val	Ile	Leu	Thr	Ala	His	Glu	Val	Thr	Gly	
			165						170					175		
Leu	Ile	Arg	Glu	Gly	Ala	Thr	Val	Cys	Gly	Val	Arg	Val	Arg	Asn	His	
			180					185					190			
Leu	Thr	Gly	Glu	Thr	Gln	Ala	Leu	His	Ala	Pro	Val	Val	Val	Asn	Ala	
	195						200					205				
Ala	Gly	Ile	Trp	Gly	Gln	His	Ile	Ala	Glu	Tyr	Ala	Asp	Leu	Arg	Ile	
	210					215					220					
Arg	Met	Phe	Pro	Ala	Lys	Gly	Ser	Leu	Leu	Ile	Met	Asp	His	Arg	Ile	
225					230					235					240	
Asn	Gln	His	Val	Ile	Asn	Arg	Cys	Arg	Lys	Pro	Ser	Asp	Ala	Asp	Ile	
			245						250					255		
Leu	Val	Pro	Gly	Asp	Thr	Ile	Ser	Leu	Ile	Gly	Thr	Thr	Ser	Leu	Arg	
		260						265					270			
Ile	Asp	Tyr	Asn	Glu	Ile	Asp	Asp	Asn	Arg	Val	Thr	Ala	Glu	Glu	Val	
	275						280					285				
Asp	Ile	Leu	Leu	Arg	Glu	Gly	Glu	Lys	Leu	Ala	Pro	Val	Met	Ala	Lys	
	290					295					300					
Thr	Arg	Ile	Leu	Arg	Ala	Tyr	Ser	Gly	Val	Arg	Pro	Leu	Val	Ala	Ser	
305					310					315					320	
Asp	Asp	Asp	Pro	Ser	Gly	Arg	Asn	Leu	Ser	Arg	Gly	Ile	Val	Leu	Leu	
			325						330					335		
Asp	His	Ala	Glu	Arg	Asp	Gly	Leu	Asp	Gly	Phe	Ile	Thr	Ile	Thr	Gly	
		340						345					350			
Gly	Lys	Leu	Met	Thr	Tyr	Arg	Leu	Met	Ala	Glu	Trp	Ala	Thr	Asp	Ala	
	355						360					365				

Val Cys Arg Lys Leu Gly Asn Thr Arg Pro Cys Thr Thr Ala Asp Leu  
 370 375 380  
 Ala Leu Pro Gly Ser Gln Glu Pro Ala Glu Val Thr Leu Arg Lys Val  
 385 390 395 400  
 Ile Ser Leu Pro Ala Pro Leu Arg Gly Ser Ala Val Tyr Arg His Gly  
 405 410 415  
 Asp Arg Thr Pro Ala Trp Leu Ser Glu Gly Arg Leu His Arg Ser Leu  
 420 425 430  
 Val Cys Glu Cys Glu Ala Val Thr Ala Gly Glu Val Gln Tyr Ala Val  
 435 440 445  
 Glu Asn Leu Asn Val Asn Ser Leu Leu Asp Leu Arg Arg Arg Thr Arg  
 450 455 460  
 Val Gly Met Gly Thr Cys Gln Gly Glu Leu Cys Ala Cys Arg Ala Ala  
 465 470 475 480  
 Gly Leu Leu Gln Arg Phe Asn Val Thr Thr Ser Ala Gln Ser Ile Glu  
 485 490 495  
 Gln Leu Ser Thr Phe Leu Asn Glu Arg Trp Lys Gly Val Gln Pro Ile  
 500 505 510  
 Ala Trp Gly Asp Ala Leu Arg Glu Ser Glu Phe Thr Arg Trp Val Tyr  
 515 520 525  
 Gln Gly Leu Cys Gly Leu Glu Lys Glu Gln Lys Asp Ala Leu  
 530 535 540

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 250 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: GPP2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Gly Leu Thr Thr Lys Pro Leu Ser Leu Lys Val Asn Ala Ala Leu  
 1 5 10 15  
 Phe Asp Val Asp Gly Thr Ile Ile Ile Ser Gln Pro Ala Ile Ala Ala  
 20 25 30  
 Phe Trp Arg Asp Phe Gly Lys Asp Lys Pro Tyr Phe Asp Ala Glu His  
 35 40 45



Val Ile Gln Val Ser His Gly Trp Arg Thr Phe Asp Ala Ile Ala Lys  
 50 55 60  
 Phe Ala Pro Asp Phe Ala Asn Glu Glu Tyr Val Asn Lys Leu Glu Ala  
 65 70 75 80  
 Glu Ile Pro Val Lys Tyr Gly Glu Lys Ser Ile Glu Val Pro Gly Ala  
 85 90 95  
 Val Lys Leu Cys Asn Ala Leu Asn Ala Leu Pro Lys Glu Lys Trp Ala  
 100 105 110  
 Val Ala Thr Ser Gly Thr Arg Asp Met Ala Gln Lys Trp Phe Glu His  
 115 120 125  
 Leu Gly Ile Arg Arg Pro Lys Tyr Phe Ile Thr Ala Asn Asp Val Lys  
 130 135 140  
 Gln Gly Lys Pro His Pro Glu Pro Tyr Leu Lys Gly Arg Asn Gly Leu  
 145 150 155 160  
 Gly Tyr Pro Ile Asn Glu Gln Asp Pro Ser Lys Ser Lys Val Val Val  
 165 170 175  
 Phe Glu Asp Ala Pro Ala Gly Ile Ala Ala Gly Lys Ala Ala Gly Cys  
 180 185 190  
 Lys Ile Ile Gly Ile Ala Thr Thr Phe Asp Leu Asp Phe Leu Lys Glu  
 195 200 205  
 Lys Gly Cys Asp Ile Ile Val Lys Asn His Glu Ser Ile Arg Val Gly  
 210 215 220  
 Gly Tyr Asn Ala Glu Thr Asp Glu Val Glu Phe Ile Phe Asp Asp Tyr  
 225 230 235 240  
 Leu Tyr Ala Lys Asp Asp Leu Leu Lys Trp  
 245 250

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 709 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: GUT1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Phe Pro Ser Leu Phe Arg Leu Val Val Phe Ser Lys Arg Tyr Ile  
 1 5 10 15

Phe	Arg	Ser	Ser	Gln	Arg	Leu	Tyr	Thr	Ser	Leu	Lys	Gln	Glu	Gln	Ser	20	25	30
Arg	Met	Ser	Lys	Ile	Met	Glu	Asp	Leu	Arg	Ser	Asp	Tyr	Val	Pro	Leu	35	40	45
Ile	Ala	Ser	Ile	Asp	Val	Gly	Thr	Thr	Ser	Ser	Arg	Cys	Ile	Leu	Phe	50	55	60
Asn	Arg	Trp	Gly	Gln	Asp	Val	Ser	Lys	His	Gln	Ile	Glu	Tyr	Ser	Thr	65	70	75
Ser	Ala	Ser	Lys	Gly	Lys	Ile	Gly	Val	Ser	Gly	Leu	Arg	Arg	Pro	Ser	85	90	95
Thr	Ala	Pro	Ala	Arg	Glu	Thr	Pro	Asn	Ala	Gly	Asp	Ile	Lys	Thr	Ser	100	105	110
Gly	Lys	Pro	Ile	Phe	Ser	Ala	Glu	Gly	Tyr	Ala	Ile	Gln	Glu	Thr	Lys	115	120	125
Phe	Leu	Lys	Ile	Glu	Glu	Leu	Asp	Leu	Asp	Phe	His	Asn	Glu	Pro	Thr	130	135	140
Leu	Lys	Phe	Pro	Lys	Pro	Gly	Trp	Val	Glu	Cys	His	Pro	Gln	Lys	Leu	145	150	155
Leu	Val	Asn	Val	Val	Gln	Cys	Leu	Ala	Ser	Ser	Leu	Leu	Ser	Leu	Gln	165	170	175
Thr	Ile	Asn	Ser	Glu	Arg	Val	Ala	Asn	Gly	Leu	Pro	Pro	Tyr	Lys	Val	180	185	190
Ile	Cys	Met	Gly	Ile	Ala	Asn	Met	Arg	Glu	Thr	Thr	Ile	Leu	Trp	Ser	195	200	205
Arg	Arg	Thr	Gly	Lys	Pro	Ile	Val	Asn	Tyr	Gly	Ile	Val	Trp	Asn	Asp	210	215	220
Thr	Arg	Thr	Ile	Lys	Ile	Val	Arg	Asp	Lys	Trp	Gln	Asn	Thr	Ser	Val	225	230	235
Asp	Arg	Gln	Leu	Gln	Leu	Arg	Gln	Lys	Thr	Gly	Leu	Pro	Leu	Leu	Ser	245	250	255
Thr	Tyr	Phe	Ser	Cys	Ser	Lys	Leu	Arg	Trp	Phe	Leu	Asp	Asn	Glu	Pro	260	265	270
Leu	Cys	Thr	Lys	Ala	Tyr	Glu	Glu	Asn	Asp	Leu	Met	Phe	Gly	Thr	Val	275	280	285
Asp	Thr	Trp	Leu	Ile	Tyr	Gln	Leu	Thr	Lys	Gln	Lys	Ala	Phe	Val	Ser	290	295	300
Asp	Val	Thr	Asn	Ala	Ser	Arg	Thr	Gly	Phe	Met	Asn	Leu	Ser	Thr	Leu	305	310	315

Lys	Tyr	Asp	Asn	Glu	Leu	Leu	Glu	Phe	Trp	Gly	Ile	Asp	Lys	Asn	Leu	325	330	335
Ile	His	Met	Pro	Glu	Ile	Val	Ser	Ser	Ser	Gln	Tyr	Tyr	Gly	Asp	Phe	340	345	350
Gly	Ile	Pro	Asp	Trp	Ile	Met	Glu	Lys	Leu	His	Asp	Ser	Pro	Lys	Thr	355	360	365
Val	Leu	Arg	Asp	Leu	Val	Lys	Arg	Asn	Leu	Pro	Ile	Gln	Gly	Cys	Leu	370	375	380
Gly	Asp	Gln	Ser	Ala	Ser	Met	Val	Gly	Gln	Leu	Ala	Tyr	Lys	Pro	Gly	385	390	395
Ala	Ala	Lys	Cys	Thr	Tyr	Gly	Thr	Gly	Cys	Phe	Leu	Leu	Tyr	Asn	Thr	405	410	415
Gly	Thr	Lys	Lys	Leu	Ile	Ser	Gln	His	Gly	Ala	Leu	Thr	Thr	Leu	Ala	420	425	430
Phe	Trp	Phe	Pro	His	Leu	Gln	Glu	Tyr	Gly	Gly	Gln	Lys	Pro	Glu	Leu	435	440	445
Ser	Lys	Pro	His	Phe	Ala	Leu	Glu	Gly	Ser	Val	Ala	Val	Ala	Gly	Ala	450	455	460
Val	Val	Gln	Trp	Leu	Arg	Asp	Asn	Leu	Arg	Leu	Ile	Asp	Lys	Ser	Glu	465	470	475
Asp	Val	Gly	Pro	Ile	Ala	Ser	Thr	Val	Pro	Asp	Ser	Gly	Gly	Val	Val	485	490	495
Phe	Val	Pro	Ala	Phe	Ser	Gly	Leu	Phe	Ala	Pro	Tyr	Trp	Asp	Pro	Asp	500	505	510
Ala	Arg	Ala	Thr	Ile	Met	Gly	Met	Ser	Gln	Phe	Thr	Thr	Ala	Ser	His	515	520	525
Ile	Ala	Arg	Ala	Ala	Val	Glu	Gly	Val	Cys	Phe	Gln	Ala	Arg	Ala	Ile	530	535	540
Leu	Lys	Ala	Met	Ser	Ser	Asp	Ala	Phe	Gly	Glu	Gly	Ser	Lys	Asp	Arg	545	550	555
Asp	Phe	Leu	Glu	Glu	Ile	Ser	Asp	Val	Thr	Tyr	Glu	Lys	Ser	Pro	Leu	565	570	575
Ser	Val	Leu	Ala	Val	Asp	Gly	Gly	Met	Ser	Arg	Ser	Asn	Glu	Val	Met	580	585	590
Gln	Ile	Gln	Ala	Asp	Ile	Leu	Gly	Pro	Cys	Val	Lys	Val	Arg	Arg	Ser	595	600	605
Pro	Thr	Ala	Glu	Cys	Thr	Ala	Leu	Gly	Ala	Ala	Ile	Ala	Ala	Asn	Met	610	615	620

Ala Phe Lys Asp Val Asn Glu Arg Pro Leu Trp Lys Asp Leu His Asp  
625 630 635 640

Val Lys Lys Trp Val Phe Tyr Asn Gly Met Glu Lys Asn Glu Gln Ile  
645 650 655

Ser Pro Glu Ala His Pro Asn Leu Lys Ile Phe Arg Ser Glu Ser Asp  
660 665 670

Asp Ala Glu Arg Arg Lys His Trp Lys Tyr Trp Glu Val Ala Val Glu  
675 680 685

Arg Ser Lys Gly Trp Leu Lys Asp Ile Glu Gly Glu His Glu Gln Val  
690 695 700

Leu Glu Asn Phe Gln  
705

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12145 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PHK28-26

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTCCGACCACC ACGGTGGTGA CTTTAATGCC GCTCTCATGC AGCAGCTCGG TGGCGGTCTC	60
AAAATTCAGG ATGTCGCCGG TATAGTTTTT GATAATCAGC AAGACGCCTT CGCCGCCGTC	120
AATTTGCATC GCGCATTCAA ACATTTTGTC CGGCGTCGGC GAGGTGAATA TTTCCCCCGG	180
ACAGGCGCCG GAGAGCATGC CCTGGCCGAT ATAGCCGCAG TGCATCGGTT CATGTCCGCT	240
GCCGCCGCCG GAGAGCAGGG CCACCTTGCC AGCCACCGGC GCGTCGGTGC GGGTCACATA	300
CAGCGGGTCC TGATGCAGGG TCAGCTGCGG ATGGGCTTTA GCCAGCCCCT GTAATTGTTC	360
ATTCAGTACA TCTTCAACAC GGTTAATCAG CTTTTTCATT ATTCAGTGCT CCGTTGGAGA	420
AGGTTTCGATG CCGCCTCTCT GCTGGCGGAG GCGGTCATCG CGTAGGGGTA TCGTCTGACG	480
GTGGAGCGTG CCTGGCGATA TGATGATTCT GGCTGAGCGG ACGAAAAAAA GAATGCCCCG	540
ACGATCGGGT TTCATTACGA AACATTGCTT CCTGATTTTG TTTCTTTATG GAACGTTTTT	600
GCTGAGGATA TGGTGAAAAT GCGAGCTGGC GCGCTTTTTT TCTTCTGCCA TAAGCGGCGG	660
TCAGGATAGC CGGCGAAGCG GGTGGGAAAA AATTTTTTGC TGATTTTCTG CCGACTGCGG	720

GAGAAAAGGC	GGTCAAAACAC	GGAGGATTGT	AAGGGCATT	TGCGGCAAAG	GAGCGGATCG	780
GGATCGCAAT	CCTGACAGAG	ACTAGGGTTT	TTTGTTC	TATGGAACGT	AAAAAATTAA	840
CCTGTGTTTC	ATATCAGAAC	AAAAAGGCGA	AAGATTTTTT	TGTTCCCTGC	CGGCCCTACA	900
GTGATCGCAC	TGCTCCGGTA	CGCTCCGTTC	AGGCCGCGCT	TCCTGGCCG	GCGCGGATAA	960
CGCCAGGGCT	CATCATGTCT	ACATGCGCAC	TTATTTGAGG	GTGAAAGGAA	TGCTAAAAGT	1020
TATTCAATCT	CCAGCCAAAT	ATCTTCAGGG	TCCTGATGCT	GCTGTTCTGT	TCGGTCAATA	1080
TGCCAAAAAC	CTGGCGGAGA	GCTTCTTCGT	CATCGCTGAC	GATTTCTGTA	TGAAGCTGGC	1140
GGGAGAGAAA	GTGGTGAATG	GCCTGCAGAG	CCACGATATT	CGCTGCCATG	CGGAACGGTT	1200
TAACGGCGAA	TGCAGCCATG	CGGAAATCAA	CCGTCTGATG	GCGATTTTGC	AAAAACAGGG	1260
CTGCCGCGGC	GTGGTCGGGA	TCGGCGGTGG	TAAAACCTC	GATACCGCGA	AGGCGATCGG	1320
TTACTACCAG	AAGCTGCCGG	TGGTGGTGAT	CCCGACCATC	GCCTCGACCG	ATGCGCCAAC	1380
CAGCGCGCTG	TCGGTGATCT	ACACCGAAGC	GGGCGAGTTT	GAAGAGTATC	TGATCTATCC	1440
GAAAAACCCG	GATATGGTGG	TGATGGACAC	GGCGATTATC	GCCAAAGCGC	CGGTACGCCT	1500
GCTGGTCTCC	GGCATGGGCG	ATGCGCTCTC	CACCTGGTTC	GAGGCCAAAG	CTTGCTACGA	1560
TGCGCGCGCC	ACCAGCATGG	CCGGAGGACA	GTCCACCGAG	GCGGCGCTGA	GCCTCGCCCCG	1620
CCTGTGCTAT	GATACGCTGC	TGGCGGAGGG	CGAAAAGGCC	CGTCTGGCGG	CGCAGGCCGG	1680
GGTAGTGACC	GAAGCGCTGG	AGCGCATCAT	CGAGGCGAAC	ACTTACCTCA	GCGGCATTGG	1740
CTTTGAAAGC	AGTGGCCTGG	CCGCTGCCCA	TGCAATCCAC	AACGGTTTCA	CCATTCTTGA	1800
AGAGTGCCAT	CACCTGTATC	ACGGTGAGAA	AGTGGCCTTC	GGTACCCTGG	CGCAGCTGGT	1860
GCTGCAGAAC	AGCCCGATGG	ACGAGATTGA	AACGGTGCAG	GGCTTCTGCC	AGCGCGTCGG	1920
CCTGCCGGTG	ACGCTCGCGC	AGATGGGCGT	CAAAGAGGGG	ATCGACGAGA	AAATCGCCGC	1980
GGTGGCGAAA	GCTACCTGCG	CGGAAGGGGA	AACCATCCAT	AATATGCCGT	TTGCGGTGAC	2040
CCCGGAGAGC	GTCCATGCCG	CTATCCTCAC	CGCCGATCTG	TTAGGCCAGC	AGTGGCTGGC	2100
GCGTTAATTC	GCGGTGGCTA	AACCGCTGGC	CCAGGTCAGC	GGTTTTTCTT	TCTCCCTCC	2160
GGCAGTCGCT	GCCGGAGGGG	TTCTCTATGG	TACAACGCGG	AAAAGGATAT	GACTGTTCAG	2220
ACTCAGGATA	CCGGGAAGGC	GGTCTCTTCC	GTCATTGCC	AGTCATGGCA	CCGCTGCAGC	2280
AAGTTTATGC	AGCGCGAAAC	CTGGCAAACG	CCGCACCAGG	CCCAGGGCCT	GACCTTCGAC	2340
TCCATCTGTC	GGCGTAAAC	CGCGCTGCTC	ACCATCGGCC	AGGCGGCGCT	GGAAGACGCC	2400

TGGGAGTTTA	TGGACGGCCG	CCCCTGCGCG	CTGTTTATTC	TTGATGAGTC	CGCCTGCATC	2460
CTGAGCCGTT	GCGGCGAGCC	GCAAACCCTG	GCCCAGCTGG	CTGCCCTGGG	ATTTCGCGAC	2520
GGCAGCTATT	GTGCGGAGAG	CATTATCGGC	ACCTGCGCGC	TGTCGCTGGC	CGCGATGCAG	2580
GGCCAGCCGA	TCAACACCGC	CGGCGATCGG	CATTTTAAGC	AGGCGCTACA	GCCATGGAGT	2640
TTTTGCTCGA	CGCCGGTGTT	TGATAACCAC	GGGCGGCTGT	TCGGCTCTAT	CTCGCTTTGC	2700
TGTCTGGTCG	AGCACCAGTC	CAGCGCCGAC	CTCTCCCTGA	CGCTGGCCAT	CGCCCCGCGAG	2760
GTGGGTAACT	CCCTGCTTAC	CGACAGCCTG	CTGGCGGAAT	CCAACCGTCA	CCTCAATCAG	2820
ATGTACGGCC	TGCTGGAGAG	CATGGACGAT	GGGGTGATGG	CGTGGAACGA	ACAGGGCGTG	2880
CTGCAGTTTC	TCAATGTTCA	GGCGGCGAGA	CTGCTGCATC	TTGATGCTCA	GGCCAGCCAG	2940
GGGAAAAATA	TCGCCGATCT	GGTGACCCTC	CCGGCGCTGC	TGCGCCGCGC	CATCAAACAC	3000
GCCCCGCGCC	TGAATCACGT	CGAAGTCACC	TTTGAAAGTC	AGCATCAGTT	TGTCGATGCG	3060
GTGATCACCT	TAAAACCGAT	TGTCGAGGCG	CAAGGCAACA	GTTTTATTCT	GCTGCTGCAT	3120
CCGGTGGAGC	AGATGCGGCA	GCTGATGACC	AGCCAGCTCG	GTAAAGTCAG	CCACACCTTT	3180
GAGCAGATGT	CTGCCGACGA	TCCGGAAACC	CGACGCCTGA	TCCACTTTGG	CCGCCAGGCG	3240
GCGCGCGGCG	GCTTCCCCGT	GCTACTGTGC	GGCGAAGAGG	GGGTCGGGAA	AGAGCTGCTG	3300
AGCCAGGCTA	TTCACAATGA	AAGCGAACGG	GCGGGCGGCC	CCTACATCTC	CGTCAACTGC	3360
CAGCTATATG	CCGACAGCGT	GCTGGGCCAG	GACTTTATGG	GCAGCGCCCC	TACCGACGAT	3420
GAAAATGGTC	GCCTGAGCCG	CCTTGAGCTG	GCCAACGGCG	GCACCCTGTT	TCTGGAAAAG	3480
ATCGAGTATC	TGGCGCCGGA	GCTGCAGTCG	GCTCTGCTGC	AGGTGATTAA	GCAGGGCGTG	3540
CTCACCCGCC	TCGACGCCCC	GCGCCTGATC	CCGGTGGATG	TGAAGGTGAT	TGCCACCACC	3600
ACCGTCGATC	TGGCCAATCT	GGTGGAACAG	AACCGCTTTA	GCCGCCAGCT	GTAATATGCG	3660
CTGCACTCCT	TTGAGATCGT	CATCCCGCCG	CTGCGCGCCC	GACGCAACAG	TATTCCGTCG	3720
CTGGTGATA	ACCGGTTGAA	GAGCCTGGAG	AAGCGTTTCT	CTTCGCGACT	GAAAGTGGAC	3780
GATGACGCGC	TGGCACAGCT	GGTGGCCTAC	TCGTGGCCGG	GGAATGATTT	TGAGCTCAAC	3840
AGCGTCATTG	AGAATATCGC	CATCAGCAGC	GACAACGGCC	ACATTTCGCT	GAGTAATCTG	3900
CCGGAATATC	TCTTTTCCGA	GCGGCCGGGC	GGGGATAGCG	CGTCATCGCT	GCTGCCGGCC	3960
AGCCTGACTT	TTAGCGCCAT	CGAAAAGGAA	GCTATTATTC	ACGCCGCCCC	GGTGACCAGC	4020
GGGCGGGTGC	AGGAGATGTC	GCAGCTGCTC	AATATCGGCC	GCACCACCCT	GTGGCGCAAA	4080
ATGAAGCAGT	ACGATATTGA	CGCCAGCCAG	TTCAAGCGCA	AGCATCAGGC	CTAGTCTCTT	4140

CGATTTCGCGC	CATGGAGAAC	AGGGCATCCG	ACAGGCGATT	GCTGTAGCGT	TTGAGCGCGT	4200
CGCGCAGCGG	ATGCGCGCGG	TCCATGGCCG	TCAGCAGGCG	TTGAGCCGA	CGGGACTGGG	4260
TGCGGCCAC	GTGCAGCTGG	GCAGAGGCGA	GATTCCTCCC	CGGGATCACG	AACTGTTTTA	4320
ACGGGCCGCT	CTCGGCCATA	TTGCGGTCGA	TAAGCCGCTC	CAGGGCGGTG	ATCTCCTCTT	4380
CGCCGATCGT	CTGGCTCAGG	CGGGTCAGGC	CCC CGCATC	GCTGGCCAGT	TCAGCCCCCA	4440
GCACGAACAG	CGTCTGCTGA	ATATGGTGCA	GGCTTTCCCG	CAGCCCGGCG	TCGCGGGTCG	4500
TGGCGTAGCA	GACGCCCAGC	TGGGATATCA	GTTTCATCGAC	GGTGCCGTAG	GCCTCGACGC	4560
GAATATGGTC	TTTCTCGATG	CGGCTGCCGC	CGTACAGGGC	GGTGGTGCCT	TTATCCCCGG	4620
TGCGGGTATA	GATACGATAC	ATTCAGTTTC	TCTCACTTAA	CGGCAGGACT	TTAACCAGCT	4680
GCCCCGCGTT	GGCGCCGAGC	GTACGCAGTT	GATCGTCGCT	ATCGGTGACG	TGTCCGGTAG	4740
CCAGCGGCGC	GTCCGCCGGC	AGCTGGGCAT	GAGTGAGGGC	TATCTCGCCG	GACGCGCTGA	4800
GCCCCGATACC	CACCCGCAGG	GGCGAGCTTC	TGGCCGCCAG	GGCGCCAGC	GCAGCGGCGT	4860
CACCGCCTCC	GTCATAGGTT	ATGGTCTGGC	AGGGGACCCC	CTGCTCCTCC	AGCCCCCAGC	4920
ACAGCTCATT	GATGGCGCCG	GCATGGTGCC	CGCGCGGATC	GTAAACAGG	CGTACGCCTG	4980
GCGGTGAAAG	CGACATGACG	GTCCCTCGT	TAACACTCAG	AATGCCTGGC	GGAAAATCGC	5040
GGCAATCTCC	TGCTCGTTGC	CTTTACGCGG	GTTTCGAGAAC	GCATTGCCGT	CTTTTAGAGC	5100
CATCTCCGCC	ATGTAGGGGA	AGTCGGCCTC	TTTTACCCCC	AGATCGCGCA	GATGCTGCGG	5160
AATACCGATA	TCCATCGACA	GACGCGTGAT	AGCGGCGATG	GCTTTTTCCG	CCGCGTCGAG	5220
AGTGGACAGT	CCGGTGATAT	TTTCGCCCAT	CAGTTCAGCG	ATATCGGCGA	ATTTCTCCGG	5280
GTTGGCGATC	AGGTTGTAGC	GCGCCACATG	CGGCAGCAGG	ACAGCGTTGG	CCACGCCGTG	5340
CGGCATGTCTG	TACAGGCCGC	CCAGCTGGTG	CGCCATGGCG	TGCACGTAGC	CGAGGTTGGC	5400
GTTATTGAAA	GCCATCCCGG	CCAGCAGAGA	AGCATAGGCC	ATGTTTTCCC	GCGCCTGCAG	5460
ATTGCTGCCG	AGGGCCACGG	CCTGGCGCAG	GTTGCGGGCG	ATGAGGCGGA	TCGCCTGCAT	5520
GGCGGCGGCG	TCCGTCACCG	GGTTAGCGTC	TTTGGAGATA	TAGGCCTCTA	CGGCGTGGGT	5580
CAGGGCATCC	ATCCCGGTCTG	CCGCGGTCTAG	GGCGGCGGTT	TTACCGATCA	TCAGCAGTGG	5640
ATCGTTGATA	GAGACCGACG	GCAGTTTGCG	CCAGCTGACG	ATCACAAACT	TCACTTTGGT	5700
TTCGGTGTTG	GTCAGGACGC	AGTGGCGGGT	GACCTCGCTG	GCGGTGCCGG	CGGTGGTATT	5760
GACCGCGACG	ATAGGCGGCA	GCGGGTTGGT	CAGGGTCTCG	ATTCCGGCAT	ACTGGTACAG	5820

ATCGCCCTCA	TGGGTGGCGG	CGATGCCGAT	GCCTTTGCCG	CAATCGTGCG	GGCTGCCGCC	5880
CCCCACGGTG	ACGATGATGT	CGCACTGTTC	GCGGCGAAAC	ACGGCGAGGC	CGTCGCGCAC	5940
GTTGGTGTCT	TTCGGGTTCG	GCTCGACGCC	GTCAAAGATC	GCCACCTCGA	TCCCGGCCTC	6000
CCGCAGATAA	TGCAGGGTTT	TGTCCACCGC	GCCATCTTTA	ATTGCCC GCA	GGCCTTTGTC	6060
GGTGACCAGC	AGGGCTTTTT	TCCCCCCCAG	CAGCTGGCAG	CGTTCGCCGA	CTACGGAAAT	6120
GGCGTTGGGG	CCAAAAAAGT	TAACGTTTGG	CACCAGATAA	TCAAACATAC	GATAGCTCAT	6180
AATATACCTT	CTCGCTTCAG	GTTATAATGC	GGAAAAACAA	TCCAGGGCGC	ACTGGGCTAA	6240
TAATTGATCC	TGCTCGACCG	TACCGCCGCT	AACGCCGACG	GCGCCAATTA	CCTGCTCATT	6300
AAAAATAACT	GGCAGGCCGC	CGCCAAAAAT	AATAATTCGC	TGTTGGTTGG	TTAGCTGCAG	6360
ACCGTACAGA	GATTGTCCTG	GCTGGACCGC	TGACGTAATT	TCATGGGTAC	CTTGCTTCAG	6420
GCTGCAGGCG	CTCCAGGCTT	TATTCAGGGA	AATATCGCAG	CTGGAGACGA	AGGCCTCGTC	6480
CATCCGCTGG	ATAAGCAGCG	TGTTGCCTCC	GCGGTCAACT	ACGGAAAAACA	CCACCGCCAC	6540
GTTGATCTCA	GTGGCTTTTT	TTTCCACCGC	CGCCGCCATT	TGCTGGGCGG	CGGCCAGGGT	6600
GATTGTCTGA	ACTTGTGGC	TCTTGTTTAT	CATTCTCTCC	CGCACCAGGA	TAACGCTGGC	6660
GCGAATAGTC	AGTAGGGGGC	GATAGTAAAA	AACTATTACC	ATTCCGGTTGG	CTTGCTTTAT	6720
TTTTGTGACG	GTTATTTTGT	CGCCCGCCAT	GATTTAGTCA	ATAGGGTTAA	AATAGCGTCG	6780
GAAAAACGTA	ATTAAGGGCG	TTTTTTATTA	ATTGATTTAT	ATCATTGCGG	GCGATCACAT	6840
TTTTTATTTT	TGCCGCCGGA	GTAAAGTTTC	ATAGTGAAAC	TGTCGGTAGA	TTTCGTGTGC	6900
CAAATTGAAA	CGAAATTAAA	TTTATTTTTT	TCACCACTGG	CTCATTTAAA	GTTCCGCTAT	6960
TGCCGGTAAT	GGCCGGGCGG	CAACGACGCT	GGCCCGGCGT	ATTCGCTACC	GTCTGCGGAT	7020
TTCACCTTTT	GAGCCGATGA	ACAATGAAAA	GATCAAAACG	ATTTGCAGTA	CTGGCCCAGC	7080
GCCCCGTCAA	TCAGGACGGG	CTGATTGGCG	AGTGGCCTGA	AGAGGGGCTG	ATCGCCATGG	7140
ACAGCCCCTT	TGACCCGGTC	TCTTCAGTAA	AAGTGGACAA	CGGTCTGATC	GTCGAACTGG	7200
ACGGCAAACG	CCGGGACCAG	TTTGACATGA	TCGACCGATT	TATCGCCGAT	TACGCGATCA	7260
ACGTTGAGCG	CACAGAGCAG	GCAATGCGCC	TGGAGGCGGT	GGAAATAGCC	CGTATGCTGG	7320
TGGATATTCA	CGTCAGCCGG	GAGGAGATCA	TTGCCATCAC	TACCGCCATC	ACGCCGGCCA	7380
AAGCGGTCGA	GGTGATGGCG	CAGATGAACG	TGGTGGAGAT	GATGATGGCG	CTGCAGAAGA	7440
TGCGTGCCCC	CCGGACCCCC	TCCAACCAGT	GCCACGTCAC	CAATCTCAAA	GATAATCCGG	7500
TGCAGATTGC	CGCTGACGCC	GCCGAGGCCG	GGATCCGCGG	CTTCTCAGAA	CAGGAGACCA	7560



CGGTCGGTAT	CGCGCGCTAC	GCGCCGTTTA	ACGCCCTGGC	GCTGTTGGTC	GGTTCGCAGT	7620
GCGGCCGCCC	CGGCGTGTTG	ACGCAGTGCT	CGGTGGAAGA	GGCCACCGAG	CTGGAGCTGG	7680
GCATGCGTGG	CTTAACCAGC	TACGCCGAGA	CGGTGTCGGT	CTACGGCACC	GAAGCGGTAT	7740
TTACCGACGG	CGATGATACG	CCGTGGTCAA	AGGCGTTCCT	CGCCTCGGCC	TACGCCTCCC	7800
GCGGGTTGAA	AATGCGCTAC	ACCTCCGGCA	CCGGATCCGA	AGCGCTGATG	GGCTATTTCGG	7860
AGAGCAAGTC	GATGCTCTAC	CTCGAATCGC	GCTGCATCTT	CATTACTAAA	GGCGCCGGGG	7920
TTCAGGGACT	GCAAAACGGC	GCGGTGAGCT	GTATCGGCAT	GACCGGCGCT	GTGCCGTCGG	7980
GCATTGCGGC	GGTGCTGGCG	GAAAACCTGA	TCGCCTCTAT	GCTCGACCTC	GAAGTGGCGT	8040
CCGCCAACGA	CCAGACTTTC	TCCCCTCGG	ATATTGCGCC	CACCGCGCGC	ACCCTGATGC	8100
AGATGCTGCC	GGGCACCGAC	TTTATTTTCT	CCGGCTACAG	CGCGGTGCCG	AACTACGACA	8160
ACATGTTTCG	CGGCTCGAAC	TTTCGATGCG	AAGATTTTGA	TGATTACAAC	ATCCTGCAGC	8220
GTGACCTGAT	GGTTGACGGC	GGCCTGCGTC	CGGTGACCGA	GGCGGAAACC	ATTGCCATTC	8280
GCCAGAAAGC	GGCGCGGGCG	ATCCAGGCGG	TTTTCCGCGA	GCTGGGGCTG	CCGCCAATCG	8340
CCGACGAGGA	GGTGGAGGCC	GCCACCTACG	CGCACGGCAG	CAACGAGATG	CCGCCGCGTA	8400
ACGTGGTGGA	GGATCTGAGT	GCGGTGGAAG	AGATGATGAA	GCGCAACATC	ACCGGCCTCG	8460
ATATTGTCGG	CGCGCTGAGC	CGCAGCGGCT	TTGAGGATAT	CGCCAGCAAT	ATTCTCAATA	8520
TGCTGCGCCA	GCGGGTCACC	GGCGATTACC	TGCAGACCTC	GGCCATTCTC	GATCGGCAGT	8580
TCGAGGTGGT	GAGTGCGGTC	AACGACATCA	ATGACTATCA	GGGGCCGGGC	ACCGGCTATC	8640
GCATCTCTGC	CGAACGCTGG	GCGGAGATCA	AAAATATTCC	GGGCGTGTTT	CAGCCCGACA	8700
CCATTGAATA	AGGCGGTATT	CCTGTGCAAC	AGACAACCCA	AATTCAGCCC	TCTTTTACCC	8760
TGAAAACCCG	CGAGGGCGGG	GTAGCTTCTG	CCGATGAACG	CGCCGATGAA	GTGGTGATCG	8820
GCGTCGGCCC	TGCCTTCGAT	AAACACCAGC	ATCACACTCT	GATCGATATG	CCCCATGGCG	8880
CGATCCTCAA	AGAGCTGATT	GCCGGGGTGG	AAGAAGAGGG	GCTTCACGCC	CGGGTGGTGC	8940
GCATTCTGCG	CACGTCCGAC	GTCTCCTTTA	TGGCCTGGGA	TGCGGCCAAC	CTGAGCGGCT	9000
CGGGGATCGG	CATCGGTATC	CAGTCGAAGG	GGACCACGGT	CATCCATCAG	CGCGATCTGC	9060
TGCCGCTCAG	CAACCTGGAG	CTGTTCTCCC	AGGCGCCGCT	GCTGACGCTG	GAGACCTACC	9120
GGCAGATTGG	CAAAAACGCT	GCGCGCTATG	CGCGCAAAGA	GTCACCTTCG	CCGGTGCCGG	9180
TGGTGAACGA	TCAGATGGTG	CGGCCGAAAT	TTATGGCCAA	AGCCGCGCTA	TTTCATATCA	9240

AAGAGACCAA	ACATGTGGTG	CAGGACGCCG	AGCCCGTCAC	CCTGCACATC	GA	CTTAGTAA	9300	
GGGAGTGACC	ATGAGCGAGA	AAACCATGCG	CGTGCAGGAT	TATCCGTTAG	CC	ACCCGCTG	9360	
CCCGGAGCAT	ATCCTGACGC	CTACCGGCAA	ACCATTGACC	GATATTACCC	TC	GAGAAGGT	9420	
GCTCTCTGGC	GAGGTGGGCC	CGCAGGATGT	GCGGATCTCC	CGCCAGACCC	TT	GAGTACCA	9480	
GGCGCAGATT	GCCGAGCAGA	TGCAGCGCCA	TGCGGTGGCG	CGCAATTTCC	GCC	GCGCGGC	9540	
GGAGCTTATC	GCCATTCCCTG	ACGAGCGCAT	TCTGGCTATC	TATAACGCGC	TG	CGCCCGTT	9600	
CCGCTCCTCG	CAGGCGGAGC	TGCTGGCGAT	CGCCGACGAG	CTGGAGCACA	CCT	GGCATGC	9660	
GACAGTGAAT	GCCGCCTTTG	TCCGGGAGTC	GGCGGAAGTG	TATCAGCAGC	GG	CATAAGCT	9720	
GCGTAAAGGA	AGCTAAGCGG	AGGTCAGCAT	GCCGTTAATA	GCCGGGATTG	AT	ATCGGCAA	9780	
CGCCACCACC	GAGGTGGCGC	TGGCGTCCGA	CTACCCGCAG	GCGAGGGCGT	TT	GTTGCCAG	9840	
CGGGATCGTC	GCGACGACGG	GCATGAAAGG	GACGCGGGAC	AATATCGCCG	GG	ACCCTCGC	9900	
CGCGCTGGAG	CAGGCCCTGG	CGAAAAACACC	GTGGTCGATG	AGCGATGTCT	CT	CGCATCTA	9960	
TCTTAACGAA	GCCGCGCCGG	TGATTGGCGA	TGTGGCGATG	GAGACCATCA	CC	GAGACCAT	10020	
TATCACCGAA	TCGACCATGA	TCGGTCATAA	CCCGCAGACG	CCGGGCGGGG	TG	GGCGTTGG	10080	
CGTGGGGACG	ACTATCGCCC	TCGGGCGGCT	GGCGACGCTG	CCGGCGGGCG	AG	TATGCCGA	10140	
GGGGTGGATC	GTA	CTGATTG	ACGACGCCGT	CGATTTCCCTT	GAC	GCCGTGT	GGTGGCTCAA	10200
TGAGGCGCTC	GACCGGGGGA	TCAACGTGGT	GGCGGCGATC	CTCAAAAAGG	AC	GACGGCGT	10260	
GCTGGTGAAC	AACCGCCTGC	GTAAAACCTT	GCCGGTGGTG	GATGAAGTGA	CG	CTGCTGGA	10320	
GCAGGTCCCC	GAGGGGGTAA	TGGCGGCGGT	GGAAGTGGCC	GCGCCGGGCC	AG	GTGGTGCG	10380	
GATCCTGTCTG	AATCCCTACG	GGATCGCCAC	CTTCTTCGGG	CTAAGCCCGG	AAG	AGACCCA	10440	
GGCCATCGTC	CCCATCGCCC	GCGCCCTGAT	TGGCAACCGT	TCCGCGGTGG	TG	CTCAAGAC	10500	
CCCGCAGGGG	GATGTGCAGT	CGCGGGTGAT	CCCGGCGGGC	AACCTCTACA	TT	AGCGGCGA	10560	
AAAGCGCCGC	GGAGAGGCCG	ATGTCGCCGA	GGGCGCGGAA	GCCATCATGC	AG	GCGATGAG	10620	
CGCCTGCGCT	CCGGTACGCG	ACATCCGCGG	CGAACCGGGC	ACCCACGCCG	GCG	GCGATGCT	10680	
TGAGCGGGTG	CGCAAGGTAA	TGGCGTCCCT	GACCGGCCAT	GAGATGAGCG	CG	ATATACAT	10740	
CCAGGATCTG	CTGGCGGTGG	ATACGTTTAT	TCCGCGCAAG	GTGCAGGGCG	GG	ATGGCCGG	10800	
CGAGTGCGCC	ATGGAGAATG	CCGTCGGGAT	GGCGGCGATG	GTGAAAGCGG	AT	CGTCTGCA	10860	
AATGCAGGTT	ATCGCCCGCG	AACTGAGCGC	CCGACTGCAG	ACCGAGGTGG	TG	GTGGGCGG	10920	
CGTGGAGGCC	AACATGGCCA	TCGCCGGGGC	GTTAACC	ACT	CCCGGCTGTG	CGGCGCCGCT	10980	

GGCGATCCTC	GACCTCGGCG	CCGGCTCGAC	GGATGCGGCG	ATCGTCAACG	CGGAGGGGCA	11040
GATAACGGCG	GTCCATCTCG	CCGGGGCGGG	GAATATGGTC	AGCCTGTTGA	TTAAAACCGA	11100
GCTGGGCCTC	GAGGATCTTT	CGCTGGCGGA	AGCGATAAAA	AAATACCCGC	TGGCCAAAGT	11160
GGAAAGCCTG	TTCAGTATTC	GTCACGAGAA	TGGCGCGGTG	GAGTTCTTTC	GGGAAGCCCT	11220
CAGCCCCGCG	GTGTTGCGCA	AAGTGGTGTA	CATCAAGGAG	GGCGAACTGG	TGCCGATCGA	11280
TAACGCCAGC	CCGCTGGAAA	AAATTCTGTCT	CGTGCGCCGG	CAGGCGAAAAG	AGAAAAGTGTT	11340
TGTCACCAAC	TGCCTGCGCG	CGCTGCGCCA	GGTCTCACCC	GGCGGTTCCA	TTCGCGATAT	11400
CGCCTTTGTG	GTGCTGGTGG	GCGGCTCATC	GCTGGACTTT	GAGATCCCGC	AGCTTATCAC	11460
GGAAGCCTTG	TCGCACTATG	GCGTGGTCGC	CGGGCAGGGC	AATATTCGGG	GAACAGAAGG	11520
GCCGCGCAAT	GCGGTCGCCA	CCGGGCTGCT	ACTGGCCGGT	CAGGCGAATT	AAACGGGCGC	11580
TCGCGCCAGC	CTCTCTCTTT	AACGTGCTAT	TTCAGGATGC	CGATAATGAA	CCAGACTTCT	11640
ACCTTAACCG	GGCAGTGCGT	GGCCGAGTTT	CTTGGCACCG	GATTGCTCAT	TTTCTTCGGC	11700
GCGGGCTGCG	TCGCTGCGCT	GCGGGTCGCC	GGGGCCAGCT	TTGGTCAGTG	GGAGATCAGT	11760
ATTATCTGGG	GCCTTGCGGT	CGCCATGGCC	ATCTACCTGA	CGGCCGGTGT	CTCCGGCGCG	11820
CACCTAAATC	CGGCGGTGAC	CATTGCCCTG	TGGCTGTTTC	CCTGTTTTGA	ACGCCGCAAG	11880
GTGCTGCCGT	TTATTGTTGC	CCAGACGGCC	GGGGCCTTCT	GCGCCGCCGC	GCTGGTGTAT	11940
GGGCTCTATC	GCCAGCTGTT	TCTCGATCTT	GAACAGAGTC	AGCATATCGT	GCGCGGCACT	12000
GCCGCCAGTC	TTAACCTGGC	CGGGGTCTTT	TCCACGTACC	CGCATCCACA	TATCACTTTT	12060
ATACAAGCGT	TTGCCGTGGA	GACCACCATC	ACGGCAATCC	TGATGGCGAT	GATCATGGCC	12120
CTGACCGACG	ACGGCAACGG	AATTC				12145

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AGCTTAGGAG	TCTAGAATAT	TGAGCTCGAA	TTCCCGGGCA	TGCGGTACCG	GATCCAGAAA	60
AAAGCCCGCA	CCTGACAGTG	CGGGCTTTTT	TTTT			94

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGAATTCAGA TCTCAGCAAT GAGCGAGAAA ACCATGC

37

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCTCTAGATT AGCTTCCTTT ACGCAGC

27

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGCCAAGCTT AAGGAGGTTA ATTAAATGAA AAG

33

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCTCTAGATT ATTCAATGGT GTCGGG

26

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCGCCGTCTA GAATTATGAG CTATCGTATG TTTGATTATC TG

42

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TCTGATACGG GATCCTCAGA ATGCCTGGCG GAAAAAT

36

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 51 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GCGCGGATCC AGGAGTCTAG AATTATGGGA TTGACTACTA AACCTCTATC T

51

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GATACGCCCCG GGTTACCATT TCAACAGATC GTCCTT

36

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TCGACGAATT CAGGAGGA

18

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTAGTCCTCC TGAATTCG

18

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CTAGTAAGGA GGACAATTC

19

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CATGGAATTG TCCTCCTTA

19

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 271 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: GPP1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met	Lys	Arg	Phe	Asn	Val	Leu	Lys	Tyr	Ile	Arg	Thr	Thr	Lys	Ala	Asn	
1				5					10					15		
Ile	Gln	Thr	Ile	Ala	Met	Pro	Leu	Thr	Thr	Lys	Pro	Leu	Ser	Leu	Lys	
			20					25					30			
Ile	Asn	Ala	Ala	Leu	Phe	Asp	Val	Asp	Gly	Thr	Ile	Ile	Ile	Ser	Gln	
		35					40					45				
Pro	Ala	Ile	Ala	Ala	Phe	Trp	Arg	Asp	Phe	Gly	Lys	Asp	Lys	Pro	Tyr	
	50					55					60					
Phe	Asp	Ala	Glu	His	Val	Ile	His	Ile	Ser	His	Gly	Trp	Arg	Thr	Tyr	
65					70					75					80	
Asp	Ala	Ile	Ala	Lys	Phe	Ala	Pro	Asp	Phe	Ala	Asp	Glu	Glu	Tyr	Val	
				85					90					95		
Asn	Lys	Leu	Glu	Gly	Glu	Ile	Pro	Glu	Lys	Tyr	Gly	Glu	His	Ser	Ile	
		100						105					110			
Glu	Val	Pro	Gly	Ala	Val	Lys	Leu	Cys	Asn	Ala	Leu	Asn	Ala	Leu	Pro	
	115						120					125				
Lys	Glu	Lys	Trp	Ala	Val	Ala	Thr	Ser	Gly	Thr	Arg	Asp	Met	Ala	Lys	
	130					135					140					
Lys	Trp	Phe	Asp	Ile	Leu	Lys	Ile	Lys	Arg	Pro	Glu	Tyr	Phe	Ile	Thr	
145					150				155					160		
Ala	Asn	Asp	Val	Lys	Gln	Gly	Lys	Pro	His	Pro	Glu	Pro	Tyr	Leu	Lys	
				165					170					175		
Gly	Arg	Asn	Gly	Leu	Gly	Phe	Pro	Ile	Asn	Glu	Gln	Asp	Pro	Ser	Lys	
		180						185					190			
Ser	Lys	Val	Val	Val	Phe	Glu	Asp	Ala	Pro	Ala	Gly	Ile	Ala	Ala	Gly	
	195						200					205				
Lys	Ala	Ala	Gly	Cys	Lys	Ile	Val	Gly	Ile	Ala	Thr	Thr	Phe	Asp	Leu	
	210					215					220					
Asp	Phe	Leu	Lys	Glu	Lys	Gly	Cys	Asp	Ile	Ile	Val	Lys	Asn	His	Glu	
225					230					235					240	

Ser Ile Arg Val Gly Glu Tyr Asn Ala Glu Thr Asp Glu Val Glu Leu  
 245 250 255

Ile Phe Asp Asp Tyr Leu Tyr Ala Lys Asp Asp Leu Leu Lys Trp  
 260 265 270

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: DHAB1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Lys Arg Ser Lys Arg Phe Ala Val Leu Ala Gln Arg Pro Val Asn  
 1 5 10 15

Gln Asp Gly Leu Ile Gly Glu Trp Pro Glu Glu Gly Leu Ile Ala Met  
 20 25 30

Asp Ser Pro Phe Asp Pro Val Ser Ser Val Lys Val Asp Asn Gly Leu  
 35 40 45

Ile Val Glu Leu Asp Gly Lys Arg Arg Asp Gln Phe Asp Met Ile Asp  
 50 55 60

Arg Phe Ile Ala Asp Tyr Ala Ile Asn Val Glu Arg Thr Glu Gln Ala  
 65 70 75 80

Met Arg Leu Glu Ala Val Glu Ile Ala Arg Met Leu Val Asp Ile His  
 85 90 95

Val Ser Arg Glu Glu Ile Ile Ala Ile Thr Thr Ala Ile Thr Pro Ala  
 100 105 110

Lys Ala Val Glu Val Met Ala Gln Met Asn Val Val Glu Met Met Met  
 115 120 125

Ala Leu Gln Lys Met Arg Ala Arg Arg Thr Pro Ser Asn Gln Cys His  
 130 135 140

Val Thr Asn Leu Lys Asp Asn Pro Val Gln Ile Ala Ala Asp Ala Ala  
 145 150 155 160

Glu Ala Gly Ile Arg Gly Phe Ser Glu Gln Glu Thr Thr Val Gly Ile  
 165 170 175

Ala Arg Tyr Ala Pro Phe Asn Ala Leu Ala Leu Leu Val Gly Ser Gln  
 180 185 190



Cys	Gly	Arg	Pro	Gly	Val	Leu	Thr	Gln	Cys	Ser	Val	Glu	Glu	Ala	Thr	195	200	205	
Glu	Leu	Glu	Leu	Gly	Met	Arg	Gly	Leu	Thr	Ser	Tyr	Ala	Glu	Thr	Val	210	215	220	
Ser	Val	Tyr	Gly	Thr	Glu	Ala	Val	Phe	Thr	Asp	Gly	Asp	Asp	Thr	Pro	225	230	235	240
Trp	Ser	Lys	Ala	Phe	Leu	Ala	Ser	Ala	Tyr	Ala	Ser	Arg	Gly	Leu	Lys	245	250	255	
Met	Arg	Tyr	Thr	Ser	Gly	Thr	Gly	Ser	Glu	Ala	Leu	Met	Gly	Tyr	Ser	260	265	270	
Glu	Ser	Lys	Ser	Met	Leu	Tyr	Leu	Glu	Ser	Arg	Cys	Ile	Phe	Ile	Thr	275	280	285	
Lys	Gly	Ala	Gly	Val	Gln	Gly	Leu	Gln	Asn	Gly	Ala	Val	Ser	Cys	Ile	290	295	300	
Gly	Met	Thr	Gly	Ala	Val	Pro	Ser	Gly	Ile	Arg	Ala	Val	Leu	Ala	Glu	305	310	315	320
Asn	Leu	Ile	Ala	Ser	Met	Leu	Asp	Leu	Glu	Val	Ala	Ser	Ala	Asn	Asp	325	330	335	
Gln	Thr	Phe	Ser	His	Ser	Asp	Ile	Arg	Arg	Thr	Ala	Arg	Thr	Leu	Met	340	345	350	
Gln	Met	Leu	Pro	Gly	Thr	Asp	Phe	Ile	Phe	Ser	Gly	Tyr	Ser	Ala	Val	355	360	365	
Pro	Asn	Tyr	Asp	Asn	Met	Phe	Ala	Gly	Ser	Asn	Phe	Asp	Ala	Glu	Asp	370	375	380	
Phe	Asp	Asp	Tyr	Asn	Ile	Leu	Gln	Arg	Asp	Leu	Met	Val	Asp	Gly	Gly	385	390	395	400
Leu	Arg	Pro	Val	Thr	Glu	Ala	Glu	Thr	Ile	Ala	Ile	Arg	Gln	Lys	Ala	405	410	415	
Ala	Arg	Ala	Ile	Gln	Ala	Val	Phe	Arg	Glu	Leu	Gly	Leu	Pro	Pro	Ile	420	425	430	
Ala	Asp	Glu	Glu	Val	Glu	Ala	Ala	Thr	Tyr	Ala	His	Gly	Ser	Asn	Glu	435	440	445	
Met	Pro	Pro	Arg	Asn	Val	Val	Glu	Asp	Leu	Ser	Ala	Val	Glu	Glu	Met	450	455	460	
Met	Lys	Arg	Asn	Ile	Thr	Gly	Leu	Asp	Ile	Val	Gly	Ala	Leu	Ser	Arg	465	470	475	480
Ser	Gly	Phe	Glu	Asp	Ile	Ala	Ser	Asn	Ile	Leu	Asn	Met	Leu	Arg	Gln	485	490	495	

Arg Val Thr Gly Asp Tyr Leu Gln Thr Ser Ala Ile Leu Asp Arg Gln  
500 505 510

Phe Glu Val Val Ser Ala Val Asn Asp Ile Asn Asp Tyr Gln Gly Pro  
515 520 525

Gly Thr Gly Tyr Arg Ile Ser Ala Glu Arg Trp Ala Glu Ile Lys Asn  
530 535 540

Ile Pro Gly Val Val Gln Pro Asp Thr Ile Glu  
545 550 555

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: DHAB2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met Gln Gln Thr Thr Gln Ile Gln Pro Ser Phe Thr Leu Lys Thr Arg  
1 5 10 15

Glu Gly Gly Val Ala Ser Ala Asp Glu Arg Ala Asp Glu Val Val Ile  
20 25 30

Gly Val Gly Pro Ala Phe Asp Lys His Gln His His Thr Leu Ile Asp  
35 40 45

Met Pro His Gly Ala Ile Leu Lys Glu Leu Ile Ala Gly Val Glu Glu  
50 55 60

Glu Gly Leu His Ala Arg Val Val Arg Ile Leu Arg Thr Ser Asp Val  
65 70 75 80

Ser Phe Met Ala Trp Asp Ala Ala Asn Leu Ser Gly Ser Gly Ile Gly  
85 90 95

Ile Gly Ile Gln Ser Lys Gly Thr Thr Val Ile His Gln Arg Asp Leu  
100 105 110

Leu Pro Leu Ser Asn Leu Glu Leu Phe Ser Gln Ala Pro Leu Leu Thr  
115 120 125

Leu Glu Thr Tyr Arg Gln Ile Gly Lys Asn Ala Ala Arg Tyr Ala Arg  
130 135 140

Lys Glu Ser Pro Ser Pro Val Pro Val Val Asn Asp Gln Met Val Arg  
145 150 155 160

Pro Lys Phe Met Ala Lys Ala Ala Leu Phe His Ile Lys Glu Thr Lys  
165 170 175

His Val Val Gln Asp Ala Glu Pro Val Thr Leu His Ile Asp Leu Val  
180 185 190

Arg Glu

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 140 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: DHAB3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Ser Glu Lys Thr Met Arg Val Gln Asp Tyr Pro Leu Ala Thr Arg  
1 5 10 15

Cys Pro Glu His Ile Leu Thr Pro Thr Gly Lys Pro Leu Thr Asp Ile  
20 25 30

Thr Leu Glu Lys Val Leu Ser Gly Glu Val Gly Pro Gln Asp Val Arg  
35 40 45

Ile Ser Arg Gln Thr Leu Glu Tyr Gln Ala Gln Ile Ala Glu Gln Met  
50 55 60

Gln His Ala Val Ala Arg Asn Phe Arg Arg Ala Ala Glu Leu Ile Ala  
65 70 75 80

Ile Pro Asp Glu Arg Ile Leu Ala Ile Tyr Asn Ala Leu Arg Pro Phe  
85 90 95

Arg Ser Ser Gln Ala Glu Leu Leu Ala Ile Ala Asp Glu Leu Glu His  
100 105 110

Thr Trp His Ala Thr Val Asn Ala Ala Phe Val Arg Glu Ser Ala Glu  
115 120 125

Val Tyr Gln Gln Arg His Lys Leu Arg Lys Gly Ser  
130 135 140

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 387 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: DHAT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met	Ser	Tyr	Arg	Met	Phe	Asp	Tyr	Leu	Val	Pro	Asn	Val	Asn	Phe	Phe	
1				5					10					15		
Gly	Pro	Asn	Ala	Ile	Ser	Val	Val	Gly	Glu	Arg	Cys	Gln	Leu	Leu	Gly	
			20					25					30			
Gly	Lys	Lys	Ala	Leu	Leu	Val	Thr	Asp	Lys	Gly	Leu	Arg	Ala	Ile	Lys	
		35					40					45				
Asp	Gly	Ala	Val	Asp	Lys	Thr	Leu	His	Tyr	Leu	Arg	Glu	Ala	Gly	Ile	
	50					55					60					
Glu	Val	Ala	Ile	Phe	Asp	Gly	Val	Glu	Pro	Asn	Pro	Lys	Asp	Thr	Asn	
65					70					75					80	
Val	Arg	Asp	Gly	Leu	Ala	Val	Phe	Arg	Arg	Glu	Gln	Cys	Asp	Ile	Ile	
				85					90					95		
Val	Thr	Val	Gly	Gly	Gly	Ser	Pro	His	Asp	Cys	Gly	Lys	Gly	Ile	Gly	
			100					105					110			
Ile	Ala	Ala	Thr	His	Glu	Gly	Asp	Leu	Tyr	Gln	Tyr	Ala	Gly	Ile	Glu	
		115					120						125			
Thr	Leu	Thr	Asn	Pro	Leu	Pro	Pro	Ile	Val	Ala	Val	Asn	Thr	Thr	Ala	
	130						135						140			
Gly	Thr	Ala	Ser	Glu	Val	Thr	Arg	His	Cys	Val	Leu	Thr	Asn	Thr	Glu	
145					150					155					160	
Thr	Lys	Val	Lys	Phe	Val	Ile	Val	Ser	Trp	Arg	Lys	Leu	Pro	Ser	Val	
			165						170					175		
Ser	Ile	Asn	Asp	Pro	Leu	Leu	Met	Ile	Gly	Lys	Pro	Ala	Ala	Leu	Thr	
			180					185						190		
Ala	Ala	Thr	Gly	Met	Asp	Ala	Leu	Thr	His	Ala	Val	Glu	Ala	Tyr	Ile	
		195					200					205				
Ser	Lys	Asp	Ala	Asn	Pro	Val	Thr	Asp	Ala	Ala	Ala	Met	Gln	Ala	Ile	
	210					215						220				
Arg	Leu	Ile	Ala	Arg	Asn	Leu	Arg	Gln	Ala	Val	Ala	Leu	Gly	Ser	Asn	
225					230					235					240	
Leu	Gln	Ala	Arg	Glu	Asn	Met	Ala	Tyr	Ala	Ser	Leu	Leu	Ala	Gly	Met	
				245					250					255		

Ala Phe Asn Asn Ala Asn Leu Gly Tyr Val His Ala Met Ala His Gln  
260 265 270

Leu Gly Gly Leu Tyr Asp Met Pro His Gly Val Ala Asn Ala Val Leu  
275 280 285

Leu Pro His Val Ala Arg Tyr Asn Leu Ile Ala Asn Pro Glu Lys Phe  
290 295 300

Ala Asp Ile Ala Glu Leu Met Gly Glu Asn Ile Thr Gly Leu Ser Thr  
305 310 315 320

Leu Asp Ala Ala Glu Lys Ala Ile Ala Ala Ile Thr Arg Leu Ser Met  
325 330 335

Asp Ile Gly Ile Pro Gln His Leu Arg Asp Leu Gly Val Lys Glu Ala  
340 345 350

Asp Phe Pro Tyr Met Ala Glu Met Ala Leu Lys Asp Gly Asn Ala Phe  
355 360 365

Ser Asn Pro Arg Lys Gly Asn Glu Gln Glu Ile Ala Ala Ile Phe Arg  
370 375 380

Gln Ala Phe  
385

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GCGAATTCAT GAGCTATCGT ATGTTTG

27

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GCGAATTCAG AATGCCTGGC GGAAAATC

28

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GGGAATTCAT GAGCGAGAAA ACCATGCG

28

- (2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GCGAATTCTT AGCTTCCTTT ACGCAGC

27

- (2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GCGAATTCAT GCAACAGACA ACCCAAATTC

30

- (2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GCGAATTCAC TCCCTTACTA AGTCG

25

- (2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGGAATTCAT GAAAAGATCA AAACGATTTG

30

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GCGAATTCTT ATTCAATGGT GTCGGGCTG

29

(2) INFORMATION FOR SEQ ID NO:46

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TTGATAATAT AACCATGGCT GCTGCTGCTG ATAG

34

(2) INFORMATION FOR SEQ ID NO:47

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTATGATATG TTATCTTGGA TCCAATAAAT CTAATCTTC

39

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CATGACTAGT AAGGAGGACA ATTC

24

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CATGGAATTG TCCTCCTTAC TAGT

24

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 94 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AGCTTAGGAG TCTAGAATAT TGAGCTCGAA TTCCCGGGCA TGCGGTACCG GATCCAGAAA

60

AAAGCCCGCA CCTGACAGTG CGGGCTTTTT TTTT

94

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGAATTCAGA TCTCAGCAAT GAGCGAGAAA ACCATGC

37

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs



- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GCTCTAGATT AGCTTCCTTT ACGCAGC

27

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGCCAAGCTT AAGGAGGTTA ATTAAATGAA AAG

33

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GCTCTAGATT ATTCAATGGT GTCGGG

26

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GCGCCGTCTA GAATTATGAG CTATCGTATG TTTGATTATC TG

42

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TCTGATACGG GATCCTCAGA ATGCCTGGCG GAAAAAT

36

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TCGACGAATT CAGGAGGA

18

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CTAGTCCTCC TGAATTCG

18

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 607 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Met	Pro	Leu	Ile	Ala	Gly	Ile	Asp	Ile	Gly	Asn	Ala	Thr	Thr	Glu	Val
1				5					10					15	
Ala	Leu	Ala	Ser	Asp	Tyr	Pro	Gln	Ala	Arg	Ala	Phe	Val	Ala	Ser	Gly
			20					25					30		
Ile	Val	Ala	Thr	Thr	Gly	Met	Lys	Gly	Thr	Arg	Asp	Asn	Ile	Ala	Gly
		35				40					45				
Thr	Leu	Ala	Ala	Leu	Glu	Gln	Ala	Leu	Ala	Lys	Thr	Pro	Trp	Ser	Met
	50				55					60					
Ser	Asp	Val	Ser	Arg	Ile	Tyr	Leu	Asn	Glu	Ala	Ala	Pro	Val	Ile	Gly
65					70				75					80	

Asp	Val	Ala	Met	Glu	Thr	Ile	Thr	Glu	Thr	Ile	Ile	Thr	Glu	Ser	Thr	85	90	95
Met	Ile	Gly	His	Asn	Pro	Gln	Thr	Pro	Gly	Gly	Val	Gly	Val	Gly	Val	100	105	110
Gly	Thr	Thr	Ile	Ala	Leu	Gly	Arg	Leu	Ala	Thr	Leu	Pro	Ala	Ala	Gln	115	120	125
Tyr	Ala	Glu	Gly	Trp	Ile	Val	Leu	Ile	Asp	Asp	Ala	Val	Asp	Phe	Leu	130	135	140
Asp	Ala	Val	Trp	Trp	Leu	Asn	Glu	Ala	Leu	Asp	Arg	Gly	Ile	Asn	Val	145	150	155
Val	Ala	Ala	Ile	Leu	Lys	Lys	Asp	Asp	Gly	Val	Leu	Val	Asn	Asn	Arg	165	170	175
Leu	Arg	Lys	Thr	Leu	Pro	Val	Val	Asp	Glu	Val	Thr	Leu	Leu	Glu	Gln	180	185	190
Val	Pro	Glu	Gly	Val	Met	Ala	Ala	Val	Glu	Val	Ala	Ala	Pro	Gly	Gln	195	200	205
Val	Val	Arg	Ile	Leu	Ser	Asn	Pro	Tyr	Gly	Ile	Ala	Thr	Phe	Phe	Gly	210	215	220
Leu	Ser	Pro	Glu	Glu	Thr	Gln	Ala	Ile	Val	Pro	Ile	Ala	Arg	Ala	Leu	225	230	235
Ile	Gly	Asn	Arg	Ser	Ala	Val	Val	Leu	Lys	Thr	Pro	Gln	Gly	Asp	Val	245	250	255
Gln	Ser	Arg	Val	Ile	Pro	Ala	Gly	Asn	Leu	Tyr	Ile	Ser	Gly	Glu	Lys	260	265	270
Arg	Arg	Gly	Glu	Ala	Asp	Val	Ala	Glu	Gly	Ala	Glu	Ala	Ile	Met	Gln	275	280	285
Ala	Met	Ser	Ala	Cys	Ala	Pro	Val	Arg	Asp	Ile	Arg	Gly	Glu	Pro	Gly	290	295	300
Thr	His	Ala	Gly	Gly	Met	Leu	Glu	Arg	Val	Arg	Lys	Val	Met	Ala	Ser	305	310	315
Leu	Thr	Gly	His	Glu	Met	Ser	Ala	Ile	Tyr	Ile	Gln	Asp	Leu	Leu	Ala	325	330	335
Val	Asp	Thr	Phe	Ile	Pro	Arg	Lys	Val	Gln	Gly	Gly	Met	Ala	Gly	Glu	340	345	350
Cys	Ala	Met	Glu	Asn	Ala	Val	Gly	Met	Ala	Ala	Met	Val	Lys	Ala	Asp	355	360	365
Arg	Leu	Gln	Met	Gln	Val	Ile	Ala	Arg	Glu	Leu	Ser	Ala	Arg	Leu	Gln	370	375	380

Thr Glu Val Val Val Gly Gly Val Glu Ala Asn Met Ala Ile Ala Gly  
 385 390 395 400  
 Ala Leu Thr Thr Pro Gly Cys Ala Ala Pro Leu Ala Ile Leu Asp Leu  
 405 410 415  
 Gly Ala Gly Ser Thr Asp Ala Ala Ile Val Asn Ala Glu Gly Gln Ile  
 420 425 430  
 Thr Ala Val His Leu Ala Gly Ala Gly Asn Met Val Ser Leu Leu Ile  
 435 440 445  
 Lys Thr Glu Leu Gly Leu Glu Asp Leu Ser Leu Ala Glu Ala Ile Lys  
 450 455 460  
 Lys Tyr Pro Leu Ala Lys Val Glu Ser Leu Phe Ser Ile Arg His Glu  
 465 470 475 480  
 Asn Gly Ala Val Glu Phe Phe Arg Glu Ala Leu Ser Pro Ala Val Phe  
 485 490 495  
 Ala Lys Val Val Tyr Ile Lys Glu Gly Glu Leu Val Pro Ile Asp Asn  
 500 505 510  
 Ala Ser Pro Leu Glu Lys Ile Arg Leu Val Arg Arg Gln Ala Lys Glu  
 515 520 525  
 Lys Val Phe Val Thr Asn Cys Leu Arg Ala Leu Arg Gln Val Ser Pro  
 530 535 540  
 Gly Gly Ser Ile Arg Asp Ile Ala Phe Val Val Leu Val Gly Gly Ser  
 545 550 555 560  
 Ser Leu Asp Phe Glu Ile Pro Gln Leu Ile Thr Glu Ala Leu Ser His  
 565 570 575  
 Tyr Gly Val Val Ala Gly Gln Gly Asn Ile Arg Gly Thr Glu Gly Pro  
 580 585 590  
 Arg Asn Ala Val Ala Thr Gly Leu Leu Leu Ala Gly Gln Ala Asn  
 595 600 605

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 142 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Met Asn Lys Ser Gln Gln Ile Ala Thr Ile Thr Leu Ala Ala Ala Lys  
 1 5 10 15

Lys	Met	Ala	Gln	Ala	Val	Glu	Ala	Lys	Ala	Leu	Glu	Ile	Asn	Val	Pro	20	25	30
Val	Val	Phe	Ser	Val	Val	Asp	His	Gly	Gly	Asn	Thr	Leu	Leu	Met	Gln	35	40	45
Arg	Met	Asp	Asp	Ala	Phe	Val	Thr	Ser	Cys	Asp	Ile	Ser	Leu	Asn	Lys	50	55	60
Ala	Tyr	Thr	Ala	Cys	Cys	Leu	Arg	Gln	Gly	Thr	His	Glu	Ile	Thr	Asp	65	70	75
Ala	Val	Gln	Pro	Gly	Ala	Ser	Leu	Tyr	Gly	Leu	Gln	Leu	Thr	Asn	Gln	85	90	95
Gln	Arg	Ile	Val	Ile	Phe	Gly	Gly	Gly	Leu	Pro	Val	Ile	Leu	Asn	Gly	100	105	110
Lys	Val	Ile	Gly	Ala	Val	Gly	Val	Ser	Gly	Gly	Thr	Val	Glu	Gln	Asp	115	120	125
Arg	Leu	Leu	Ala	Glu	Thr	Ala	Leu	Asp	Cys	Phe	Ser	Glu	Leu			130	135	140

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 143 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Met	Met	Asn	Lys	Ser	Gln	Gln	Val	Gln	Thr	Ile	Thr	Leu	Ala	Ala	Ala	1	5	10	15
Gln	Gln	Met	Ala	Ala	Ala	Val	Glu	Lys	Lys	Ala	Thr	Glu	Ile	Asn	Val	20	25	30	
Ala	Val	Val	Phe	Ser	Val	Val	Asp	Arg	Gly	Gly	Asn	Thr	Leu	Leu	Ile	35	40	45	
Gln	Arg	Met	Asp	Glu	Ala	Phe	Val	Ser	Ser	Cys	Asp	Ile	Ser	Leu	Asn	50	55	60	
Lys	Ala	Trp	Ser	Ala	Cys	Ser	Leu	Lys	Gln	Gly	Thr	His	Glu	Ile	Thr	65	70	75	80
Ser	Ala	Val	Gln	Pro	Gly	Gln	Ser	Leu	Tyr	Gly	Leu	Gln	Leu	Thr	Asn	85	90	95	
Gln	Gln	Arg	Ile	Ile	Ile	Phe	Gly	Gly	Gly	Leu	Pro	Val	Ile	Phe	Asn	100	105	110	

Glu Gln Val Ile Gly Ala Val Gly Val Ser Gly Gly Thr Val Glu Gln  
115 120 125

Asp Gln Leu Leu Ala Gln Cys Ala Leu Asp Cys Phe Ser Ala Leu  
130 135 140

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 117 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met Ser Leu Ser Ser Pro Gly Val His Leu Phe Tyr His Ser Arg Trp  
1 5 10 15

Gln Gly Thr Arg Val Leu Asp Glu Leu Cys Trp Gly Leu Glu Glu Gln  
20 25 30

Gly Val Pro Cys Arg Ala Ile Cys Cys Asp Asp His Asp Cys Ala Leu  
35 40 45

Ala Leu Gly Lys Leu Ala Ala Lys Ser Ser Thr Leu Arg Val Gly Leu  
50 55 60

Gly Leu Asn Ala Thr Gly Asp Ile Ala Leu Thr His Ala Gln Leu Pro  
65 70 75 80

Glu Asp Arg Ala Leu Val Cys Gly His Thr Arg Ala Gly Thr Ala Gln  
85 90 95

Ile Arg Thr Leu Gly Ala Asn Ala Gly Gln Leu Val Lys Val Leu Pro  
100 105 110

Phe Ser Glu Ile Lys  
115

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 117 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met Ser Leu Ser Pro Pro Gly Val Arg Leu Phe Tyr Asp Pro Arg Gly  
1 5 10 15

His His Ala Gly Ala Ile Asn Glu Leu Cys Trp Gly Leu Glu Glu Gln  
                   20                                  25                                  30  
 Gly Val Pro Cys Gln Thr Ile Thr Tyr Asp Gly Gly Gly Asp Ala Ala  
                   35                                  40                                  45  
 Ala Leu Gly Ala Leu Ala Ala Arg Ser Ser Pro Leu Arg Val Gly Ile  
                   50                                  55                                  60  
 Gly Leu Ser Ala Ser Gly Glu Ile Ala Leu Thr His Ala Gln Leu Pro  
 65                                  70                                  75                                  80  
 Ala Asp Ala Pro Leu Ala Thr Gly His Val Thr Asp Ser Asp Asp Gln  
                                   85                                  90                                  95  
 Leu Arg Thr Leu Gly Ala Asn Ala Gly Gln Leu Val Lys Val Leu Pro  
                   100                                  105                                  110  
 Leu Ser Glu Arg Asn  
                   115

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 176 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met Tyr Arg Ile Tyr Thr Arg Thr Gly Asp Lys Gly Thr Thr Ala Leu  
 1                                  5                                  10                                  15  
 Tyr Gly Gly Ser Arg Ile Glu Lys Asp His Ile Arg Val Glu Ala Tyr  
                   20                                  25                                  30  
 Gly Thr Val Asp Glu Leu Ile Ser Gln Leu Gly Val Cys Tyr Ala Thr  
                   35                                  40                                  45  
 Thr Arg Asp Ala Gly Leu Arg Glu Ser Leu His His Ile Gln Gln Thr  
                   50                                  55                                  60  
 Leu Phe Val Leu Gly Ala Glu Leu Ala Ser Asp Ala Arg Gly Leu Thr  
 65                                  70                                  75                                  80  
 Arg Leu Ser Gln Thr Ile Gly Glu Glu Glu Ile Thr Ala Leu Glu Arg  
                   85                                  90                                  95  
 Leu Ile Asp Arg Asn Met Ala Glu Ser Gly Pro Leu Lys Gln Phe Val  
                   100                                  105                                  110  
 Ile Pro Gly Arg Asn Leu Ala Ser Ala Gln Leu His Val Ala Arg Thr  
                   115                                  120                                  125

Gln Ser Arg Arg Leu Glu Arg Leu Leu Thr Ala Met Asp Arg Ala His  
 130 135 140

Pro Leu Arg Asp Ala Leu Lys Arg Tyr Ser Asn Arg Leu Ser Asp Ala  
 145 150 155 160

Leu Phe Ser Met Ala Arg Ile Glu Glu Thr Arg Pro Asp Ala Cys Ala  
 165 170 175

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 176 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met Tyr Arg Ile Tyr Thr Arg Thr Gly Asp Asn Gly Thr Thr Ala Leu  
 1 5 10 15

Phe Gly Gly Ser Arg Ile Asp Lys Asp Asp Ile Arg Val Glu Ala Tyr  
 20 25 30

Gly Thr Val Asp Glu Leu Ile Ser Gln Leu Gly Val Cys Tyr Ala Ser  
 35 40 45

Thr Arg Gln Ala Glu Leu Arg Gln Glu Leu His Ala Met Gln Lys Met  
 50 55 60

Leu Phe Val Leu Gly Ala Glu Leu Ala Ser Asp Gln Lys Gly Leu Thr  
 65 70 75 80

Arg Leu Lys Gln Arg Ile Gly Glu Glu Asp Ile Gln Ala Leu Glu Gln  
 85 90 95

Leu Ile Asp Arg Asn Met Ala Gln Ser Gly Pro Leu Lys Glu Phe Val  
 100 105 110

Ile Pro Gly Lys Asn Leu Ala Ser Ala Gln Leu His Val Ala Arg Thr  
 115 120 125

Leu Thr Arg Arg Leu Glu Arg Ile Leu Ile Ala Met Gly Arg Thr Leu  
 130 135 140

Thr Leu Arg Asp Glu Ala Arg Arg Tyr Ile Asn Arg Leu Ser Asp Ala  
 145 150 155 160

Leu Phe Ser Met Ala Arg Ile Glu Glu Thr Thr Pro Asp Val Cys Ala  
 165 170 175

(2) INFORMATION FOR SEQ ID NO:66:



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1830 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ATGCGCTATA	TCGCTGGCAT	TGATATTGGC	AACTCCTCGA	CAGAAGTCGC	CCTGGCGACG	60
GTCGATGACG	CAGGTGTGCT	GAACATTTCGC	CACAGCGCGT	TGGCTGAAAC	CACGGGTATA	120
AAAGGCACAT	TACGAAATGT	GTTCTGGTATC	CAGGAGGCGC	TAACGCAGGC	GGCAAAAGCG	180
GCCGGCATTTC	AGCTCAGCGA	TATTTTCGCTT	ATTTCGCATTA	ACGAAGCCAC	GCCGGTCATT	240
GGCGATGTGG	CGATGGAAAC	CATCACGGAA	ACCATCATCA	CCGAGTCCAC	CATGATCGGC	300
CATAACCCGA	AGACACCCGG	CGGCGTCGGA	CTGGGGGTTCG	GCATCACCAT	CACACCAGAG	360
GCGCTGCTGT	CCTGCTCCGC	GGACACTCCC	TATATTCTGG	TGGTCTCCTC	GGCCTTTGAC	420
TTTGCCGATG	TCGCCGCGAT	GGTCAATGCG	GCAACGGCAG	CGGGCTATCA	GATAACCGGC	480
ATTATTTTGC	AGCAGGATGA	CGGCGTGCTG	GTCAATAACC	GGCTACAGCA	ACCGCTACCG	540
GTGATCGACG	AAGTTCAGCA	TATCGACCGG	ATTCCACTTG	GCATGCTGGC	GGCCGTCGAG	600
GTCGCTTTAC	CCGGTAAGAT	CATCGAAACG	CTCTCCAACC	CTTACGGTAT	TGCGACCGTT	660
TTCGATCTCA	ACGCCGAGGA	GAGCCAAAAT	ATCGTGCCAA	TGGCACGGGC	GCTGATTGGC	720
AACCGCTCGG	CCGTGGTGGT	GAAAACCCCC	TCCGGCGACG	TCAAGGCCCG	CGCTATTCCG	780
GCAGGTAATC	TGTTGCTCAT	CGCTCAGGGG	CGCAGCGTAC	AGGTTGATGT	GGCCGCCGGG	840
GCGGAAGCCA	TCATGAAAGC	GGTTGACGGC	TGCGGCAAAC	TGGACAACGT	CGCGGGAGAA	900
GCGGGCACCA	ATATCGGCGG	CATGCTAGAG	CACGTGCGCC	AGACCATGGC	GGAGCTTACC	960
AATAAGCCAG	CTCAGGAGAT	CCGCATTGAG	GATCTGCTGG	CCGTTGATAC	GGCGGTGCCA	1020
GTCAGCGTGA	CCGGCGGTCT	TGCGGGGGAG	TTCTCGCTGG	AGCAGGCGGT	GGGTATCGCC	1080
TCGATGGTCA	AGTCGGATCG	CCTGCAGATG	GCCCTCATCG	CCCGTGAAAT	TGAGCACAAA	1140
CTGCAGATTG	CGGTTGAGGT	GGGCGGCGCC	GAAGCGGAGG	CGGCCATTCT	TGGGGCGCTC	1200
ACCACTCCCG	GCACCACGCG	CCCCTGGCG	ATCCTCGATC	TGGGCGCCGG	GTCGACCGAC	1260
GCCTCCATTA	TCAATGCGCA	GGGAGAGATC	AGCGCCACTC	ACCTGGCCGG	CGCCGGCGAT	1320
ATGGTCACGA	TGATCATCGC	CCGCGAGCTG	GGGCTTGAGG	ACCGCTACCT	GGCGGAAGAG	1380
ATCAAAAAAT	ATCCGCTGGC	AAAAGTCGAA	AGCCTGTTTC	ATCTGCGTCA	TGAAGACGGC	1440

AGCGTCCAGT TTTTTCCTGTC GGCCTTACCA CCGACGGTAT TTGCCCCGCGT CTGCGTGAAA 1500  
 CCGGATGAAC TGGTTCCCCCT GCCCGGCGAT CTGCCGCTGG AGAAAGTGCG CGCAATTCGC 1560  
 CGTAGCGCCA AATCACGCGT CTTTGTCACC AACGCCCTGC GAGCGTTACG CCAGGTGAGC 1620  
 CCTACCGGCA ACATTGCGA CATCCCGTTC GTGGTGCTGG TGGGCGGCTC GTCCCTCGAT 1680  
 TTCGAGATCC CCCAGCTGGT CACCGACGCG CTGGCGCACT ACCGGCTGGT TGCCGGGCGC 1740  
 GGCAACATCC GCGGCTGTGA AGGCCCCACGC AATGCGGTTCG CCAGCGGATT ACTCCTTTCC 1800  
 TGGCAAAAAG GAGGCACACA TGGAGAGTAG 1830

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 609 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met	Arg	Tyr	Ile	Ala	Gly	Ile	Asp	Ile	Gly	Asn	Ser	Ser	Thr	Glu	Val	1	5	10	15
Ala	Leu	Ala	Thr	Val	Asp	Asp	Ala	Gly	Val	Leu	Asn	Ile	Arg	His	Ser	20	25	30	
Ala	Leu	Ala	Glu	Thr	Thr	Gly	Ile	Lys	Gly	Thr	Leu	Arg	Asn	Val	Phe	35	40	45	
Gly	Ile	Gln	Glu	Ala	Leu	Thr	Gln	Ala	Ala	Lys	Ala	Ala	Gly	Ile	Gln	50	55	60	
Leu	Ser	Asp	Ile	Ser	Leu	Ile	Arg	Ile	Asn	Glu	Ala	Thr	Pro	Val	Ile	65	70	75	80
Gly	Asp	Val	Ala	Met	Glu	Thr	Ile	Thr	Glu	Thr	Ile	Ile	Thr	Glu	Ser	85	90	95	
Thr	Met	Ile	Gly	His	Asn	Pro	Lys	Thr	Pro	Gly	Gly	Val	Gly	Leu	Gly	100	105	110	
Val	Gly	Ile	Thr	Ile	Thr	Pro	Glu	Ala	Leu	Leu	Ser	Cys	Ser	Ala	Asp	115	120	125	
Thr	Pro	Tyr	Ile	Leu	Val	Val	Ser	Ser	Ala	Phe	Asp	Phe	Ala	Asp	Val	130	135	140	
Ala	Ala	Met	Val	Asn	Ala	Ala	Thr	Ala	Ala	Gly	Tyr	Gln	Ile	Thr	Gly	145	150	155	160
Ile	Ile	Leu	Gln	Gln	Asp	Asp	Gly	Val	Leu	Val	Asn	Asn	Arg	Leu	Gln				

165						170						175					
Gln	Pro	Leu	Pro	Val	Ile	Asp	Glu	Val	Gln	His	Ile	Asp	Arg	Ile	Pro		
			180					185						190			
Leu	Gly	Met	Leu	Ala	Ala	Val	Glu	Val	Ala	Leu	Pro	Gly	Lys	Ile	Ile		
		195					200						205				
Glu	Thr	Leu	Ser	Asn	Pro	Tyr	Gly	Ile	Ala	Thr	Val	Phe	Asp	Leu	Asn		
	210						215				220						
Ala	Glu	Glu	Ser	Gln	Asn	Ile	Val	Pro	Met	Ala	Arg	Ala	Leu	Ile	Gly		
225					230					235					240		
Asn	Arg	Ser	Ala	Val	Val	Val	Lys	Thr	Pro	Ser	Gly	Asp	Val	Lys	Ala		
				245					250					255			
Arg	Ala	Ile	Pro	Ala	Gly	Asn	Leu	Leu	Leu	Ile	Ala	Gln	Gly	Arg	Ser		
			260					265					270				
Val	Gln	Val	Asp	Val	Ala	Ala	Gly	Ala	Glu	Ala	Ile	Met	Lys	Ala	Val		
		275					280						285				
Asp	Gly	Cys	Gly	Lys	Leu	Asp	Asn	Val	Ala	Gly	Glu	Ala	Gly	Thr	Asn		
	290						295				300						
Ile	Gly	Gly	Met	Leu	Glu	His	Val	Arg	Gln	Thr	Met	Ala	Glu	Leu	Thr		
305					310					315					320		
Asn	Lys	Pro	Ala	Gln	Glu	Ile	Arg	Ile	Gln	Asp	Leu	Leu	Ala	Val	Asp		
				325					330					335			
Thr	Ala	Val	Pro	Val	Ser	Val	Thr	Gly	Gly	Leu	Ala	Gly	Glu	Phe	Ser		
			340					345					350				
Leu	Glu	Gln	Ala	Val	Gly	Ile	Ala	Ser	Met	Val	Lys	Ser	Asp	Arg	Leu		
		355					360						365				
Gln	Met	Ala	Leu	Ile	Ala	Arg	Glu	Ile	Glu	His	Lys	Leu	Gln	Ile	Ala		
	370						375				380						
Val	Gln	Val	Gly	Gly	Ala	Glu	Ala	Glu	Ala	Ala	Ile	Leu	Gly	Ala	Leu		
385					390					395					400		
Thr	Thr	Pro	Gly	Thr	Thr	Arg	Pro	Leu	Ala	Ile	Leu	Asp	Leu	Gly	Ala		
				405					410					415			
Gly	Ser	Thr	Asp	Ala	Ser	Ile	Ile	Asn	Ala	Gln	Gly	Glu	Ile	Ser	Ala		
			420					425					430				
Thr	His	Leu	Ala	Gly	Ala	Gly	Asp	Met	Val	Thr	Met	Ile	Ile	Ala	Arg		
		435					440						445				
Glu	Leu	Gly	Leu	Glu	Asp	Arg	Tyr	Leu	Ala	Glu	Glu	Ile	Lys	Lys	Tyr		
	450						455				460						
Pro	Leu	Ala	Lys	Val	Glu	Ser	Leu	Phe	His	Leu	Arg	His	Glu	Asp	Gly		

465	470	475	480
Ser Val Gln Phe Phe Pro Ser Ala Leu Pro Pro Thr Val Phe Ala Arg			
	485	490	495
Val Cys Val Lys Pro Asp Glu Leu Val Pro Leu Pro Gly Asp Leu Pro			
	500	505	510
Leu Glu Lys Val Arg Ala Ile Arg Arg Ser Ala Lys Ser Arg Val Phe			
	515	520	525
Val Thr Asn Ala Leu Arg Ala Leu Arg Gln Val Ser Pro Thr Gly Asn			
	530	535	540
Ile Arg Asp Ile Pro Phe Val Val Leu Val Gly Gly Ser Ser Leu Asp			
	545	550	555
Phe Glu Ile Pro Gln Leu Val Thr Asp Ala Leu Ala His Tyr Arg Leu			
	565	570	575
Val Ala Gly Arg Gly Asn Ile Arg Gly Cys Glu Gly Pro Arg Asn Ala			
	580	585	590
Val Ala Ser Gly Leu Leu Leu Ser Trp Gln Lys Gly Gly Thr His Gly			
	595	600	605

Glu

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1824 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ATGCCGTTAA TAGCCGGGAT TGATATCGGC AACGCCACCA CCGAGGTGGC GCTGGCGTCC	60
GACTACCCGC AGGCGAGGGC GTTTGTTGCC AGCGGGATCG TCGCGACGAC GGGCATGAAA	120
GGGACGCGGG ACAATATCGC CGGGACCCTC GCCGCGCTGG AGCAGGCCCT GGCGAAAACA	180
CCGTGGTCGA TGAGCGATGT CTCTCGCATC TATCTTAACG AAGCCGCGCC GGTGATTGGC	240
GATGTGGCGA TGGAGACCAT CACCGAGACC ATTATCACCG AATCGACCAT GATCGGTCAT	300
AACCCGCGA CGCCGGGCGG GGTGGGCGTT GGCGTGGGGA CGACTATCGC CCTCGGGCGG	360
CTGGCGACGC TGCCGGCGGC GCAGTATGCC GAGGGGTGGA TCGTACTGAT TGACGACGCC	420
GTCGATTTCC TTGACGCCGT GTGGTGGCTC AATGAGGCGC TCGACCGGGG GATCAACGTG	480
GTGGCGGCGA TCCTCAAAAA GGACGACGGC GTGCTGGTGA ACAACCGCCT GCGTAAACC	540

CTGCCGGTGG	TGGATGAAGT	GACGCTGCTG	GAGCAGGTCC	CCGAGGGGGT	AATGGCGGCG	600
GTGGAAGTGG	CCGCGCCGGG	CCAGGTGGTG	CGGATCCTGT	CGAATCCCTA	CGGGATCGCC	660
ACCTTCTTCG	GGCTAAGCCC	GGAAGAGACC	CAGGCCATCG	TCCCCATCGC	CCGCGCCCTG	720
ATTGGCAACC	GTTCCGCGGT	GGTGCTCAAG	ACCCCGCAGG	GGGATGTGCA	GTCGCGGGTG	780
ATCCCGGCGG	GCAACCTCTA	CATTAGCGGC	GAAAAGCGCC	GCGGAGAGGC	CGATGTCGCC	840
GAGGGCGCGG	AAGCCATCAT	GCAGGCGATG	AGCGCCTGCG	CTCCGGTACG	CGACATCCGC	900
GGCGAACCGG	GCACCCACGC	CGGCGGCATG	CTTGAGCGGG	TGCGCAAGGT	AATGGCGTCC	960
CTGACCGGCC	ATGAGATGAG	CGCGATATAC	ATCCAGGATC	TGCTGGCGGT	GGATACGTTT	1020
ATTCCGCGCA	AGGTGCAGGG	CGGGATGGCC	GGCGAGTGCG	CCATGGAGAA	TGCCGTCGGG	1080
ATGGCGGCGA	TGGTGAAAGC	GGATCGTCTG	CAAATGCAGG	TTATCGCCCC	CGAACTGAGC	1140
GCCCGACTGC	AGACCGAGGT	GGTGGTGGGC	GGCGTGAGAG	CCAACATGGC	CATCGCCGGG	1200
GCGTTAACCA	CTCCCGGCTG	TGCGGCGCCG	CTGGCGATCC	TCGACCTCGG	CGCCGGGCTCG	1260
ACGGATGCGG	CGATCGTCAA	CGCGGAGGGG	CAGATAACGG	CGGTCCATCT	CGCCGGGGCG	1320
GGGAATATGG	TCAGCCTGTT	GATTAAAACC	GAGCTGGGCC	TCGAGGATCT	TTGCTGGCG	1380
GAAGCGATAA	AAAAATACCC	GCTGGCCAAA	GTGGAAAGCC	TGTTCACTAT	TCGTACAGAG	1440
AATGGCGCGG	TGGAGTTCTT	TCGGGAAGCC	CTCAGCCCGG	CGGTGTTTCG	CAAAGTGGTG	1500
TACATCAAGG	AGGGCGAACT	GGTGCCGATC	GATAACGCCA	GCCCGCTGGA	AAAAATTCGT	1560
CTCGTGCGCC	GGCAGGCGAA	AGAGAAAGTG	TTTGTCACCA	ACTGCCTGCG	CGCGCTGCGC	1620
CAGGTCTCAC	CCGGCGGTTC	CATTGCGGAT	ATCGCCTTTG	TGGTGCTGGT	GGGCGGCTCA	1680
TCGCTGGACT	TTGAGATCCC	GCAGCTTATC	ACGGAAGCCT	TGTCGCACTA	TGGCGTGGTC	1740
GCCGGGCAGG	GCAATATTCG	GGGAACAGAA	GGGCCGCGCA	ATGCGGTCGC	CACCGGGCTG	1800
CTACTGGCCG	GTCAGGCGAA	TTAA				1824

a'  
Cmt